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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 7092, Ap
Sequence 8562, Ap
Sequence 2, Appli
Sequence 9992, Ap
Sequence 7091, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 11161, A
Sequence 11162, A
Sequence 11162, A
Sequence 44488, A
Sequence 22, Appli
Sequence 22, Appli
Sequence 24, Appli
Sequence 27, Appli
Sequence 28, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                               PATENT APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION: WITH HUMAN DISEASE, METHODS OF INTILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF INTERNIT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRSETSEQ for Windows Version 4.0
SEQ ID NO 7092
LENGTH: 508
TYPE: PRT
ORGANISM: Human
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      PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
                                  QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                                                                                                    ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
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US-09-976-767-45399

US-09-270-767-43895

US-09-270-767-43895

US-09-949-016-10078

US-09-949-016-10078

US-09-949-016-10078

US-09-949-016-10466

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US-09-949-016-7973

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Result

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SUMMARIES

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Minimum Maximum

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Total number

of hits satisfying chosen parameters:

513545 seqs, 74649064 residues

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 s

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Scoring table:

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Title: Perfect score:

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen

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Issued\_Patents\_AA:\*

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5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PRILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FRACESEQ for Windows Version 4.0

SEQ ID NO 8562

LENGTH: 508

TYPE: PRT

ORGANISM: Human

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Matches 479
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                                                                 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
                                                                                                                                                         PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVBIN 362
                                                                                                                                                                                                                           QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
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; SEQ ID NO 2
; LENGTH: 503
; TYPE: PRT
; ORGANISM: H. I
US-09-144-367-2
RESULT 4
US-09-949-016-8561
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APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09144367 Patent No. 6432639
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Best Local Similarity
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CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                               MRFALMNMKLALIRVLONFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA
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Sequence 8561, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

USES

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Sequence 5992, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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; ORGANISM: Human
US-09-949-016-8561
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Best Local Similarity
Matches 425; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Pred. No. 4.6e-217;
7; Mismatches 27;
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OF DETECTION
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GER
TITLE OF INVENTION: WITH HUWAN DISEASE, METHC
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-09-31,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOSTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7091
LENGTH: 507
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US-09-949-016-7091
; Sequence 7091, A
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                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7091
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Best Local S
Matches 402
                                                                                                     Matches
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6812339
GENERAL INFORMATION:
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Local Similarity 84.1%;
hes 402; Conservative 3
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TDPDMIKTVLVKECYSVFTNRRPFGFVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
                                                        YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
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                                          YGTRTHGLFKRLGIPGPTPLPLLGNVLSYRQGLWKFDTECYKKYGKMWGTYEGQLPVLAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application
                                                                                                     Conservative
                                                                                                               84.3%;
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                                                                                                  Score 2142.5;
Pred. No. 6.6e
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               METHODS
                                                                                                                 .6e-208;
                                                                                                                             DB 4;
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OF DETECTION
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TOPOVIRTVLVKECYSVFTNRRSLGPVGFMKSAISLAEDEEWKRIRSLLSPTFTSGKLKE

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APPLICANT: WOUNOWSKI, Leszek
APPLICANT: GELNER, Klaus
APPLICANT: EISELT, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE
TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
FILE REFERENCE: 310115.401
CURRENT APPLICATION NUMBER: US/09/583,447A
CURRENT APPLICATION NUMBER: US/09/583,447A
CURRENT EILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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US-09-583-447A-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Query Match 77.0%; Sco
Best Local Similarity 76.2%; Pro
Matches 364; Conservative 51;
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                                                               QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                                                                                                                                                                    MVPIIAQYGDVLVRNI.RREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
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                                            QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH
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Pred. No. 3.9e-189;
51; Mismatches 63;
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US-08-457-274A-25
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GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
APPLICANT: Tomita, Takashi
TITLE OF INVENTION: Cytochrome P4501pr Gene and
NUMBER OF SEQUENCES: 29
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                                                                                                                                                                           Matches
                                                                                                                                                                                                             Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: prote HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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CITY: R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                    TDPDMIKTVLVKECYSVFTNRRPFGFVGFMKSAISIAEDEBWKRLRSLLSFTFTSGKLKE 122
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MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
                                                                                                        FGTRTHGLFKKQGIPGPKPLPFFGTVLNYYMGLWKFDVECHKKYGKIWGLFDGQMPLFAI
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                                    TDTEMIKNVLVKECFSVFTNRRDFGPVGIMGKAVSVAKDEEWKRYRALLSPTFTSGRLKE
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                                                                                                                                                                                           Score 1946.5; DB 1
Pred. No. 4.5e-188;
                                                                                                                                                                           Mismatches
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APPLICANT: WOJNOWSKI, Leszek
APPLICANT: GELLMER, Klaus
APPLICANT: GELLMER, Klaus
APPLICANT: EISELT, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
FILE REFERENCE: 310115.401
CURRENT APPLICATION NUMBER: US/09/583,447A
CURRENT APPLICATION UNMBER: US/09/583,447A
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 504
TYPE: PRT
'ORGANISM: Homo sapiens
US-09-583-447A-4
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US-09-583-447A-4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFPIIEQYGDILVKYLKQEASTGKPVTMKKVFGAYSMDVITSTSFGVNVDSLNNPKDPFV
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PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN
                                                                       QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKHRVDFLQLMMNAHNDSKDKESHTALSDMEITAQSIIFIFAGYEPTSSTLSFVLHSLAT 324
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                                                                                                                                                                                                                                                                                                                                                                                                                   76.6%; Score 1946.5; DB 4; Length ilarity 76.0%; Pred. No. 4.5e-188; Conservative 51; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     504;
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ORGANISM: RAT
STRAIN: Unknown
DEVELOPMENTAL STAGE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT: U
PCT-US95-05758-25
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PCT-US95-05758-25
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                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cornell ReTITLE OF INVENTION: (TITLE OF INVENTION: UNMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: F.C. STREET: FOCHESTER CITY: Rochester CTATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
ANTI-SENSE: NO
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                                                                                                                                                                                                                    Local
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 504 amino acids
 145
                 123 MVPIIAQYGDVLVRNLRREAETGKFVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDFFV 182
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                                                                                    63 TDPDMIKTVLVKECYSVFTNRRPFGFVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
                                                                                                                                 25 FGTRTHGLEKKQGIPGPKPLPFFGTVLNYYMGLMKFDVECHKKYGKIWGLFDGQMPLFAI
                                                                                                                                                     3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
                                                                                                                                                                                                                    Similarity
 MFP11EQYGD1LVKYLKQEAETGKPVTMKKVFGAYSMDV1TSTSFGVNVDSLNNPKDPFV
                                                                TDTEMIKNVLVKECFSVFTNRRDFGPVGIMGKAVSVAKDEEWKRYRALLSPTFTSGRLKE
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                                                                                                                                                                                                 76.6%; Score 1946.5; DB 5 ilarity 74.0%; Pred. No. 4.5e-188; Conservative 62; Mismatches 62;
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204
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Sequence 6, Application US/09583447A

Patent No. 6645745

GENERAL INFORMATION:
APPLICANT: WOJNOWSKI, Leszek
APPLICANT: GELLINER, Klaus
APPLICANT: GELLINER, Klaus
APPLICANT: GELLINER, Klaus
APPLICANT: GELLINER, REGina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE
TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
FILE REFERENCE: 310115.401
CURRENT APPLICATION NUMBER: US/09/583,447A
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 420
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US-09-583-447A-6
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Best Local S
Matches 299
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TYPE: PRT
ORGANISM: Homo sapiens
-09-583-447A-6
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                                                                                                                                                      TDPDMIKTVLVKECYSVFTNRRPFGFVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
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                                                PDVQQKLQEEIDAVLPNKAPVTYDALVQMBYLDMVVNETLRLFPVVSRVTRVCKKDIEIN
                                                                  PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
                                                                                                   QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIFAAYDTTSTTLFFIMYELATH
                                                                                                                   QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                 63.7%;
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; Pred. No. 3.8e-155;
45; Mismatches 50;
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Sequence 11161, Application US/09949016

Patent No. 6812339

PATENTICATION UPPORT IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERE

PITE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PattSEQ for Windows Version 4.0

SEQ ID NO 11161

LENGTH: 554

TYPE: PRT

PROGRAISM: Human

US-09-949-016-11161
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US-09-949-016-11161
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Matches
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                                                                                                                                             CSLEEGLPYLDMVIAETLRMYPPAFRFTREAAQDCEVLGQRIPAGAVLEMAVGALHHDPE
                   PCKETQIPLKLSLGGLLQPEKPVVLKVESR 474
                                                                    HWPSPETFNPERFTAEAROOHRPFTYLPFGAGPRSCLGVRLGLLEVKLTLLHVLHKFRFQ
                                                                                                                                                                                                                                                                                             ALRDQQAAEERRRDFLQMVLDARHSASPMGVQDFDIVRDVFSSTGCKPNPSRQHQPSPMA
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ACPETOVPLOLESKSALGPKNGVYIKIVSR
                                                                                             FVKHCKRFFEFCIPRPILVLLLSFPSIMVPLARIL----PNKNRDELNGFFNKLIRNVI
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RESULT 13
US-09-949-016-11162
; Sequence 11162, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABELSEQ for Windows Version 4.
SEQ ID NO 11162
LENGTH: 554
Typer Dem
Sequence 8, Application US/09583447A

Patent No. 6645745;
GENERAL INFORMATION:
APPLICANT: WOJNOWSKI, Leszek
APPLICANT: GELLNER, Klaus
APPLICANT: EISELT, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF
TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
FILE REFERENCE: 310115.401
CURRENT APPLICATION NUMBER: US/09/583,447A
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US-09-583-447A-8
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/949,
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 46468

LENGTH: 529

TYPE: PRT
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 8
LENGTH: 250
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ORGANISM: Homo sapiens
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SIIFIFAGYETTSSVLSFIMYELATHPDVQQKLQEEIDAV---LPNKAPPTYDTVLQMEY
                                                                                                AFGLQVNSFKDRENTFYQMGKKLTTFTFLQS--MKFMLFFALKGLNKILKVELFDRKSTQ
                                                                                                                   SFGVNIDSLANDQDDFVENTKKLLRFDFLDFFFLSITVFPFLIPILEVLNICVFPREVTN : | | : :: | : : | : | : | : |
                                                                                                                                                                                                RSLLSPTFTSGKLKEMVPIIAQYGDVLVRNLRREAE---TGKPVTLKDVFGAYSMDVITST
                                                                                                                                                                                                                                                                                                WASANNDFFKDRGIAYEKPVLYFGNMAGMFLRKRAMFDIVCDLYTKGGSKKFFGIFEQRQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENTKKLLRFDFLDPFFLSI 201
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KNMKKLLKLDFLDPFLLLI 223
                                                                                                                                                                                                                                PLLMVRDPDLIKQITIKD-FDHFINHRNVFATSSDDDPHDMSNLFGSSLFSMRDARWKDM
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                                                                 -FLRKSVKRMKESRLEDTQKH---RVDFLQLMIDSQNSKETESHKA-----LSDLELVAQ
                                                                                                                                                                  {\tt RSTLSPAFTGSKMRQMFQLMNQVAKEAVDCLKQDDSRVQENELDMKDYCTRFTNDVIAST}
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                                                                                                                                                                                                                                                                                                                                                                  28.4%; Score 721.5; DB 4; 33.9%; Pred. No. 4.8e-64; tive 111; Mismatches 181;
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Pred. No. 1e-72;
23; Mismatches
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Query Match 98.4%; Score 2501; DB 2; Length 503 Best Local Similarity 100.0%; Pred. No. 3.8e-174; Matches 479; Conservative 0; Mismatches 0; Indels	GO; GO:0004497; F:monoxygenase activity; IDA. GO; GO:0004497; F:monoxygenase activity; IDA. GO; GO:0005649; F:testosterone 6-beta-hydroxylase activity; IDA. GO; GO:0005805; P:xembiotic metabolism; TAS. InterPro; IPR001128; Cytochrome_P450. InterPro; IPR002401; EP450I. InterPro; IPR008072; EP450 CYP3A. Pfam; PF00067; pF450 I. PRINTS; PR00667; EP450I. PRINTS; PR01689; EP450I. PRINTS; PR00385; P450. PRINTS; PR00385; CYTOCHROME_P450; UNKNOWN_1. Heme; Monooxygenase; Oxidoreductase. SEQUENCE 503 AA; 57394 MM; 4141F95B28B34A6E CRC64;	SUB-Liver;  LINE=21839017; PubMed=11726664; DC  LINE=21839017; PubMed=11726664; DC  ta C., Zaphiropoulos P.G.;  tergenic mRNA molecules resulting  Biol. Chem. 277:5882-5890(2002).  UENCE FROM N.A.  SUB-Liver;  hiropoulos P.G.;  hiropoulos P.G.;	RELIMINARY; P TrEMBLrel. 24, Cre IrEMBLrel. 26, Las 50, ErembLrel. 26, Las CYP3A4; (Human). (Human). (Human).	32 1884 74.1 503 1 CP3E CAVPO 33 1878.5 73.9 504 1 CP3G MOUSE 34 1877 73.8 503 1 CP3E MOUSE 35 1876 73.8 503 2 CP3E MOUSE 36 1857 73.1 503 1 CP3E CAVPO 37 1849.5 72.8 504 2 CP3E CAVPO 38 1846 72.6 503 1 CP3E CAVPO 39 1845 72.2 501 1 CP3V MESAU 40 1802 70.9 497 1 CP3I RAT 41 1788 70.3 503 1 CP3E MESAU 42 1696 66.7 353 2 CP3E MESAU 43 1596 62.8 508 2 CP5U4 44 1560.5 61.4 504 2 CP5U4 45 1550 61.0 496 1 C330_FUNHE  AllGAMPENTS  AllGAMPENTS  AllGAMPENTS  AllGAMPENTS  AllGAMPENTS  Q64417 cavia porce Q94481 mus musculu Q64406 cavia porce Q64406 cavia porce Q64407 cavia porce Q64408 cavia porce Q64408 cavia porce Q64408 cavia porce Q64409 cavia porce Q64409 cavia porce Q64409 cavia porce Q64401 mus musculu Q64401 cavia porce Q64401 rattus musculu Q64401 rattus morv Q64401 rattus musculu Q64401 rat

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01-JAN-1988 (Rel. 06, Created) 
01-NOV-1990 (Rel. 16, Last sequence update) 
05-JUL-2004 (Rel. 44, Last annotation update) 
Cytochrome P450 3A4 (EC 1.14.13.67) (Quinine 3-monooxygenase) 
(CYPIIIA4) (Nifedipine oxidase) (NF-25) (P450-PCNI).
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                      "Characterization of mRNA species related 450 nifedipine oxidase and the regulation J. Biol. Chem. 264:910-919(1989).
                                                                                                                    TISSUE=Liver;
MEDLINE=89093163; PubMed=2463251;
MEDLINE=89093163; PubMed=2463251;
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"Sequence
Submitted
                                       Biselt R., Domanski T.L., Zibat A., Mueller I
Hustert E., Zanger U.M., Brockmoller J., Kles
Khan K.K., He Y.-A., Halpert J.R., Wojnowski
                                                                                                                                                                VARIANTS GLN-161; SER-188; PRO-292; THR-444 AND SER-466, AN CHARACTERIZATION OF THE VARIANTS.
MEDLINE=21571796; PubMed=11714865;
Dai D., Tang J., Rose R., Hodgson E., Bienstock R.J.,
Mohrenweiser H.W., Goldstein J.A.;
Mohrenweiser H.W., Goldstein J.A.;
"Identification of variants of CYPJA4 and characterization abbilities to metabolize testosterone and chlorpyrifos.";
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MEDLINE=20132287; PubMed=10668853; DOI=10.1067/mcp.2000.104391;
Sata F., Sapone A., Elizondo G., Stocker P., Miller V.P., Zheng
Raunio H., Crespi C.L., Gonzalez F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                         microsomes. Evidence for metabolic pathways.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gellner K., Biselt R., Hustert E., Arnol
Deglmann C.J., Burk O., Buntefuss D., Ek
Koebe H.-G., Brinkmann U., Klenk H.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen Q., Wu J., Yu Y.; "Establishment of transgenic
protein variants.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97243737; PubMec Zhang H., Coville P.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic organization of the human CYP3A locus: identification of new, inducible CYP3A gene.";
Pharmacogenetics 11:111-121(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Liver;
                          "Identification and functional characterization
                                                                                           MEDLINE=21364010;
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                                                                                                                     VARIANTS ASP-55; GLN-129; ILE-169; HIS-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evidence for involvement of human CYP3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                         EU-415
                                                                                                                                                   Pharmacol.
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                                                                                                                                                                                                                                                                                                                                                                                                          Metab. Dispos. 26:188-191(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qian Y., Xie H., Yu Y.; of a new human cytochrome P450-3A4 cDNA."; (SEP-1999) to the EMBL/GenBank/DDBJ databa
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                                                                                                                                                   Exp.
                                                                                       PubMed=11470997;
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P.F., Walker R.J.,
                                                                                                                                                   Ther. 299:825-831(2001).
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                                                                         Zibat A., Mueller R.,
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D., Escher S., Bishop C.,
.-P., Kleine K., Meyer U.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         and etoposide by human liver
e P4503A4 involvement in thei
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                                                          J., Klenk H.-P.,
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                             eight CYP3A4
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                                                           Meyer U.A.,
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IR GO; GO:0005624; C:membrane fraction; ISS.

IR GO; GO:0005624; C:membrane fractivity; ISS.

IR GO; GO:0004497; F:monooxygenase activity; ISS.

IR GO; GO:0019825; F:oxygen binding; TAS.

IR GO; GO:0016829; F:lipid metabolism; TAS.

IR GO; GO:0006805; P:xenobiotic metabolism; ISS.

IR InterPro; IPR001128; Cytochrome P450.

IR InterPro; IPR008072; EP450 CYPSĀ.

IR InterPro; IPR008072; EP450 CYPSĀ.

IR InterPro; IPR002401; EP450I.

IR PRINTS; PR00463; EP450I.

IR PRINTS; PR00463; EP450I.

IR PRINTS; PR01689; EP450; 1.

IR PRINTS; PR00385; P450.

IR PRINTS; PR00385; P450.

IR PROSITE; PS00086; CYTOCHROME P450; 1.

IR PROSITE; PS00086; CYTOCHROME P450; 1.
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IV ARIANTS PRO-14; GLN-161; HIS-173; SER-184 AND PHE-372.

WARDLINE=21864884; PubMed=11875366;

Lamba J.K., Lin Y.S., Thummel K., Daly A., Watkins P.B., Strom S.,

A Zhang J., Schuetz E.G.;

Tommon allelic variants of cytochrome P4503A4 and their prevalence in Ciferent populations.";

Pharmacogenetics 12:121-132(2002).

1. Pharmacogenetics 12:121-132(2002).

2. I. Pharmacogenases. In liver microsomes, this enzyme is involved in an Ciferent proposed and their prevalence in Ciferent proposed and their prevalence of conceygenases. In liver microsomes, this enzyme is involved in an Ciferent proposed and their prevalence of conceygenases. In liver microsomes, this enzyme is involved in an Ciferent proposed and their prevalence of conceygenases. In liver microsomes, this enzyme is involved in an Ciferent proposed in the conceygenase of conceygenases. In liver microsomes, this enzyme is involved in an Ciferent proposed in Ciferent propose
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EMBL; M14096; AAA35744.1; -.
EMBL; X12387; CAA30944.1; -.
EMBL; J04449; AAA35747.1; -.
EMBL; AF280107; AAF312598.1; -.
EMBL; AF280107; AAG32290.1; -.
EMBL; AF209389; AAF21034.1; -.
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METAL 441
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MIM; 124010; -.
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HSSP; P14779; LJPZ.
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SIMILARITY: Belongs to the cytochrome P450 family DATABASE: NAME=Cytochrome P450 Allele Nomenclatur NOTE=CYP3A4 alleles;

WWW="http://www.imm.ki.se/CYPalleles/cyp3a4.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Membrane-bound. Endoplas TISSUB SPECIFICITY: Expressed in prostate and INDUCTION: P450 can be induced to high levels tissues by various foreign compounds, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydroxylates etoposide.
CATALYTIC ACTIVITY: Quinine + NADPH +
NADP(+) + H(2)O.
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                    FTId=VAR 011597.

G = D (in allele C)
FTId=VAR 011598.

I = V (in allele C)
FTId=VAR 011599.

R = O (in allele C)
FTId=VAR 011600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                         Iron
                                                                                                                                                                                                                        (heme axial ligand) (By P (in allele CYP3A4*14)
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Nomenclature
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CYP3A4*15)
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         MRFALMMMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA
                                                     GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG
                                                                                                  PDVQQKLQBEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
                                                                                                                              QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                                                                                                                                                                       ENTKKLLRFDFLDPFFLSITVFPFLIFILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                                                                                                                                                                   MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                                                                                                                                                                                                 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDBEWKRLRSLLSPTFTSGKLKE
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                                                                                                                                                                                                                                                                                                                     YGTHSHGLFKKLGIFGFTFLFFLGNILSYHKGFCMFDMECHKKYGKVMGFYDGQQPVLAI
                                                                                                                                                                           ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                                                                                                                                                     MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                     PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLPPIAMRLERVCKKDVEIN
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99.8%;
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F -> S (in allele CYP3A4*17; exhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                       V -> I (in allele CYP3A4*9).
/FTId=VAR_011602.
D -> H (in allele CYP3A4*10)
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L.2e-173;
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RESULT 3
CP33_HUMAN
 MEDITINE-86.829780, PubMed=3460094;
MEDITINE-86.829780, PubMed=3460094;
Mendez-Picon G., Parker G.A., Guzelian P. &
"Complete cDNA sequence of a cytochrome P. glucocorticoids in human liver.";
Proc. Natl. Acad. Sci. U.S.A. 83:5311-5311
                                                                                                                                                                                                                                                              CP33_HUMAN
P05184;
                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Cytochrome P450 3A3 (EC 1.14.14.1) (CYPIIIA3)
           SEQUENCE OF 1-20 TISSUE=Liver;
                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                   Name=CYP3A3;
                                                                                                                                                                                                                                                                           STANDARD;
PubMed=3898085
                                                                                                                                                                 Chordata;
Primates;
                                              83:5311-5315 (1986)
                                                                                                                                                               Catarrhini; Hominidae;
                                                                                                                                                                            Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                           503
                                                                    P-450 inducible
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                                                                                           Watkins
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Best Local S
Matches 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:2636; CYP3A3.
GO; GO:0005524; C:membrane fraction;
GO; GO:0005792; C:microsome; TAS.
GO; GO:0004497; P:monooxygenase activ
GO; GO:0019825; P:oxygen binding; TAS
GO; GO:0006805; P:xenobiotic metaboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001128; Cytochrome P450.
InterPro; IPR008072; EP450 CYP3Ā.
InterPro; IPR002401; EP450T.
Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP450IICYP3A.
PRINTS; PR00385; P450.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D00003; BAA00001.1;
EMBL; M13785; AAA35742.1;
PIR; A29410; A29410.
HSSP; P14779; JJPZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of structurally unrelated compounds, including steroids, fa acids, and xenobiotics.

CATIALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH oxidized flavoprotein + H(2)O.

SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: By glucocorticoids. SIMILARITY: Belongs to the cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monooxygenases. In liver microsomes, this enzyme is involved in an NADPH-dependent electron transport pathway. It oxidizes a variety of structurally unrelated compounds, including steroids, fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION:
    302
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                                                               QKHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT
                                                                                                                                        ENTKKLLRFDFLDFFFLSITVFPFLIFILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                                                                                                                                                   MVPIIAQYGDVLVRNLKREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                                                                                                                                                                                                                                 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
                                                                                                                                                                                                                                                                                                                                                                                YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
  HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI
                                        QKHRVDFLQLMIDSHKNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT
                                                                                                                                                                                               MVPIIAQYGDVLVRNLRRERETGKPVTLKDVFGAYSMDVITSSSFGVNVDSLNNPQDPLV
                                                                                                                                                                                                                                                                          TDPDMIKLVLVKECYSVFTNREPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442
503 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochromes
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P450 are a group of neme ...

T+ OX
                                                                                                                  Score 2449.5;
Pred. No. 2.2e-
4; Mismatches
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; 9B85D1F729658FC0 CRC64;
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MACFA
CP38 MACFA
STAULER
23268; P25231;
P33268; P25231;
O1-FEB-1994 (Rel. 28, Created)
O1-FEB-1994 (Rel. 28, Last sequence update)
O5-JUL-2004 (Rel. 44, Last annotation update)
O5-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                           EMBL; S53047; AAB2495;
PIR; S28168; S28168.
HSSP; P14779; JJPZ.
GO; GO:0005624; C:ment
GO; GO:0004497; F:mont
GO; GO:0006805; P:xenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytochrome P-450.";
Biochim. Biophys. Acta 996:142-145(1989).
-I- FUNCTION: Catalyzes nifedipine and nilvadipine oxidations.
-I- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH
--- oxidized flavoprotein + H(2)O.
--- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACFA
InterPro; IPR001128; Cytochrome
InterPro; IPR008072; EP455_CYP3A
InterPro; IPR002401; EP450I.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89287352; PubMed=2500151;
Ohta K., Kitada M., Hashizume T.,
"Purification of cytochrome P-450
treated crab-eating monkeys: high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komori M., Kikuchi O., Sakuma T., Funaki J., Kitada M., Kar
"Molecular cloning of monkey liver cytochrome P-450 cDNAs:
of the primary sequences to human cytochromes P-450.";
Biochim. Biophys. Acta 1171:141-146(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis
Eukaryota; Metazoa;
Mammalia; Eutheria;
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MEDLINE=93129612; PubMed=1282830;
"----- w kikuchi O., Sakuma T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9541;
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                                                                                                     GO:0005624; C:membrane fraction; ISS. GO:0004497; F:monooxygenase activity; GO:0006805; P:xenobiotic metabolism;
                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: By polychlorinated biphenyl (PCB). SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384
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Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                          .
                                                             CYP3A.
                                                                                          P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1016/0167-4838(89)90107-6;
Komori M., Ohi H., Kamataki T.;
from polychlorinated biphenyl-
homology to a form of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOI=10.1016/0167-4781(92)90113-E;
Funaki J., Kitada M., Kamataki T.;
r cytochrome P-450 cDNAs: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (P450-MKNF2) (P-450-
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PRINTS; PR01689; EP450IICYP3A PRINTS; PR00385; P450.

CYTOCHROME\_P450;

PR00463; EP450I.

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RESULT
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Best I
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                                                                                                     Booth-Genthe C.L., Rushmore T.H.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ c
-i-SIMILARITY: Belongs to the cytochrome P450
EMBL; AY334551; AAP94642.1; -.
GO; GO:0004497; F:monnooxygenase activity; IEA.
GO; GO:0016712; P:oxidoreductase activity, acti
GO; GO:0006118; P:electron transport; IEA.
            InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP4501.
InterPro; IPR0080772; EP450_CYP3A.
Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP450ICYP3A.
PRINTS; PR01689; EP450ICYP3A.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       Cercopithecinae;
                                                                                                                                                                                                                                                                                           Name=CYP3A64;
                                                                                                                                                                                                                                                                                                       Cytochrome P450 3A64.
                                                                                                                                                                                                                                                                                                                                                          Q6VP01;
                                                                                                                                                                                                                                                                                                                                                                         Q6VP01
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Heme; Membrane; Microsome;
METAL 442 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQDEKPVVLKVBSRDGTVSGA
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                                                                                                                                                                                                                                       Macaca.
CYTOCHROME_P450; UNKNOWN_1.
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93.9%;
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Monooxygenase; Oxidoreductase:
Iron (heme axial ligand) (By similarity)
MW; D701B6FE83AC8BFB CRC64;
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Last sequ
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Pred. No. 1e-164;
B; Mismatches 1
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Best Local S
Matches 450
Bukaryota, Metazoa, Chordata,
Bukaryota, Metazoa, Primates,
Mammalia, Butheria, Primates,
Carcopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-UII-2004 (TrEMBLrel. 27, Created)
05-UII-2004 (TrEMBLrel. 27, Last sequence update)
05-UII-2004 (TrEMBLrel. 27, Last annotation updat
Cytochrome P450 3A64 variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae;
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Cr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=CYP3A64;
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SEQUENCE 503 AA; 57511 MW; D701B6FE83AC8BFB
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ENTKKLLRPDFLDPFFLSITIFPFIIPILEVLNISIFPREVTSFLRKSVKRIKGSRLKDT
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Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
      E5206E2DAD8BAE28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Euteleostomi;
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Similarity

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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
Cytochrome P450 3A21 (EC 1.14.14.1) (C
                                                                                                                                                                                                                                                                                                                         Callithrix jacchus (Common marmoset)
Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Primates; Platyr
                                                                                                                                                                                                              MEDLINE=97223367; PubMed=9056237; DOI=10.1006/abbi.1996.9852; Igarashi T., Sakuma T., Isogai M., Nagata R., Kamataki T.; "Marmoset liver cytochrome P450s: study for expression and mocloning of their cDNAs.";
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Name=CYP3A21;
                              SIMILARITY:
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  SWISS-PROT
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01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cytochrome P450 3A7 (EC 1.14.14.1) (CYPIIIA7)

Name=CYP3A7; Homo sapiens Bukaryota; Me

Metazoa;

Chordata;

Craniata; Vertebrata;

Euteleostomi;

(P450-HFLA)

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37\_HUMAN CP37\_HUMAN P24462;

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R HSSP; P14779; 1JPZ.

RGO; GO:0005624; C:membrane fraction; ISS.

RGO; GO:0005624; C:membrane fraction; ISS.

RGO; GO:0004697; F:monooxygenase activity; ISS.

RGO; GO:0004897; F:monooxygenase activity; ISS.

InterPro; IPR00128; Cytochrome P450.

InterPro; IPR008072; EP450 CYP3A.

R InterPro; IPR002401; EP450 T.

R InterPro; IPR002401; EP450 T.

R Pfam; PF00067; P450; 1.

PFAm; PF00067; P450; 1.

R PRINTS; PR01689; EP450ICYP3A.

R PRINTS; PR01689; EP450ICYP3A.

R PRINTS; PR01689; EP450ICYP3A.

R PRINTS; PR00385; P450.

R PROSITE; PS00086; CYTOCHROME_P450; 1.

R PROSITE; PS00086; CYTOCHROME_P450; 1.

R PROSITE; PS00086; CYTOCHROME_P450; 1.

R PROSITE; PS00086; Oxidoreductase.

M Monooxygenase; Oxidoreductase.

IIOn (heme axial ligand) (By similarity).

R PROFITED A AA AA AN AND ABENDA TROCAGA.
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Best Local Sim
Matches 431;
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Oxidoreductase.
Iron (heme axial ligand)
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Iron (heme axial ligand)
AAA: 57564 MW; 9BFD421D72C76D6A CRC64;
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Pred. No. 3.2e-158;
6; Mismatches 22;
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Eutheria;

Primates;

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OR GO; GO:0005624; C:membrane fraction; ISS.

R GO; GO:0004497; F:monoxygenase activity; ISS.

R GO; GO:0019825; F:cxygen binding; TAS.

R GO; GO:0019805; P:xenobiotic metabolism; ISS.

InterPro; IPR001128; Cytochrome p450.

R InterPro; IPR008072; EP450 CYPJĀ.

R InterPro; IPR002401; EP450I.

R Pfam; PP00067; p450; 1.

R PRINTS; PR00463; EP450I.

R PRINTS; PR01699; EP450IICYPJA.

R PROSCITE; PS00086; CYTOCHROME P450; 1.

R PROSCITE; PS00086; CYTOCHROME P450; 1.

MODOOXYGENASE; Oxidoreductase.
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HSSP; P14779; 1JPZ.
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Gellner K., Eiselt R., Hustert B., Arnold H., Koch
Deglmann C.J., Burk O., Buntefuss D., Escher S., Bi
Koebe H.-G., Brinkmann U., Klenk H.-P., Kleine K.,
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MEDLINE=89255154; PubMed=2722762;
MEDLINE=89255154; PubMed=2722762;
Komori M., Nishio K., Ohi H., Kitada M., Kamataki T.;
"Molecular cloning and sequence analysis of cDNA containing coding region for human fetal liver cytochrome P-450.";
J. Biochem. 105:161-163(1989).
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CATALYTIC ACTIVITY: RH - reduced flavoprotein + O(2) = oxidized flavoprotein + H(2)O.

SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic retic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the cytochrome DATABASE: NAME=Cytochrome P450 Allele NOTE=CYP3A7 alleles;
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Pred. No. 1.
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; 087CCEED9BAC314C CRC64;
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       Query Match
Best Local S
Matches 421
                                                                                                                                                                                                                                                                                         HSSP; P14779; 1JPZ.
GO; GO:0005624; C:membrane fraction; ISS.
GO; GO:0004497; F:monooxygenase activity;
GO; GO:0006805; P:xenobiotic metabolism; InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                PRINTS; PR00463; EP450I.
PRINTS; PR01689; EP450IICYP3A.
PRINTS; PR00385; P450.
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InterPro; IPR008072; EP450_CYP3A.
Pfam; PF00067; p450; 1.
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01-MAR-2004 (TrEMBLrel.
Cytochrome P450 variant
                                                                                                                   PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
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Gene 260:13-23(2000)
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Mammalia; Eutheria;
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01-MAR-2001
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                                                                                                SEQUENCE
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EMBL; AF315325; AAG48618.1;
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Query Match
Best Local Similarity
Matches 430; Conserv
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Q7Z448;
Q7Z448;
01-OCT-2003 (TrEMBLrel. 25, C:
01-OCT-2003 (TrEMBLrel. 25, L:
01-MAR-2004 (TrEMBLrel. 26, L:
Cytochrome P450 (Fragment).
                                                                               Heme; Mor
NON TER
SEQUENCE
                                                                                                                                                                                                                                           Zaphiropoulos P.G.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2003) to the cytochrome P450 family. -!-SIMILARITY: Belongs to the cytochrome P450 family. EMBL; AJ563376; CAD91645.1; --
HSSP; P14779; 1JPZ.
                                                                                                                                      GO; GO:0004497; F:monooxygenase activity; I
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_
                                                                                                                                                                                                                                                                                                                                                                                       [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21839017; PubMed=11726664; DOI=10.1074/jbc.M109175200; Finta C., Zaphiropoulos P.G.; Finta C., Zaphiropoulos P.G.; "Intergenic mRNA molecules resulting from trans-splicing."; J. Biol. Chem. 277:5882-5890(2002).
                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=CYP3A4;
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                                                                                                                     Monooxygenase;
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                                                                               430
  Conservative
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Primates;
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                                                                                                      Oxidoreductase.
                     87.0%; Score 2212; DB 2 100.0%; Pred. No. 3.9e-1
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                                                                               C232BF7E2571155C
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cytochrome P-450 hPCN3, a novel cytochrome P-450 IIIA gene product that is differentially expressed in adult human liver. cDNA and deduced amino acid sequence and distinct specificities of cDNA-expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and cyclosporine.";
           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler Mitschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
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Gelboin H.V.
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length human

Tand mouse cDNA sequences.";

The Proc. Mart A.
EMBL; J04813; AAA02993.1; -.
EMBL; BC033862; AAH33862.1; -.
EMBL; BC2886.2; -AAG32288.1; -.
EMBL; L35912; AAB00083.1; -.
PIR; A34101; A34101.
HSSP; P14779; LJPZ.
Genew; HGNC:2638; CYP3A5.
                                                                                                                                                                                                                                                                 modified and this statement entities requires a line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT CYP3A5*2.

WARDLINE=96192071; PubMed=8619878; DOI=10.1006/bbrc.1996.0618;
Jounaidi Y., Hyrailles V., Gervot L., Maurel P.;
"Detection of CYP3A5 allelic variant: a candidate for the pol expression of the protein?";
Blochem. Biophys. Res. Commun. 221:466-470(1996).
Blochem. Biophys. Res. Commun. 221:466-470(1996).

-1- FUNCTION: Cytochromes P450 are a group of heme-thiolate monooxygenases. In liver microsomes, this enzyme is invol NADPH-dependent electron transport pathway. It oxidizes a of structurally unrelated compounds, including steroids,
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-106 FROM N.A.

MEDLINB=21163842; PubMed=11266076;

MEDLINB=21163842; PubMed=11266076;

Gellner K., Eiselt R., Hustert B., Arnold H., Koch I., Haberl |

Deglmann C.J., Burk O., Buntefuss D., Escher S., Bishop C.,

Deglmann C.J., Burk O., Buntefuss D., Kleine K., Meyer U.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human CYP3A5 gene and its activation Mol. Pharmacol. 49:63-72(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96152836; PubMed=8569713; Schuetz J.D., Schuetz E.G., Thottassery
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Pharmacogenetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-24 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acids, and xenobiotics.

CATALYTIC ACTIVITY: RH + reduced flavoprotein + oxidized flavoprotein + H(2)O.

SUBCELLULAR LOCATION: Membrane-bound. Endoplasmi INDUCTION: P450 can be induced to high levels in tissues by various foreign compounds, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and carcinogens.
SIMILARITY: Belongs to the DATABASE: NAME=Cytochrome NOTE=CYP3A5 alleles;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWW="http://www.imm.ki.se/CYPalleles/cyp3a5.htm".
                                                                                                                                                                                                                                           s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acad.
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cs 11:111-121(2001).
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                                                                                                                                                                                                                                                                 institutions as long as its content is catement is not removed. Usage by and for license agreement (See http://www.isb-sib.
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P450 Allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endoplasmic reticulum.
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Nomenclature
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g steroids, fatty
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J., Hulyk S.W.,
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O6GUQ3 PRELIMINARY;
Q6GUQ3;
O5-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
Cytochrome P450 CYP3A66;
Name=CYP3A66;
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MIM; 605325; -...
GO; GO:0005624; C:memi
GO; GO:0005792; C:mic:
GO; GO:0004497; F:mon
GO; GO:00019825; F:cxy;
GO; GO:0008202; P:ste:
GO; GO:0006805; P:xen
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METAL 441 441 Iron (heme axis
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PRINTS; PR01689; EP450IICYP3A.
PRINTS; PR00385; P450.
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InterPro; IPRO08072; EP450 CYP3A.
InterPro; IPRO08010; EP450I.
Pfam; PF00067; P450; 1.
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GO:0005792; C:microsome; TAS.
GO:0004497; F:monooxygenase a
GO:0019825; F:oxygen binding;
GO:0008202; P:steroid metaboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0006805; P:xenobiotic metabolism;
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                                                                                                                                                  MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
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C:microsome; TAS.
F:monooxygenase activity;
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Pred. No. 5.8
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annotation updat
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Best Local 9
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01-MAR-1992
01-MAR-1992
05-JUL-2004
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InterPro; IPR002401; EP450I.
InterPro; IPR008072; EP450_CYP3A.
Pfam; PF00067; P450; 1.
PRINTS; PR01689; EP450IICYP3A.
PRINTS; PR01689; EP450IICYP3A.
PRINTS; PR00385; P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Carr B.A., Fang Y., Rushmore T.H.;

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                         Cytochrome P450
Name=CYP3A12;
   Eukaryota;
               Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
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NCE 503 AA; 57382 MW; DOB!
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                                                                                                                                                            MRFALMNMKLALIRVLQNESFKPCKETQIPLKLSLGGILQPEKPVVLKVESRDGTVSG
                                                                                                                                                                                                          QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                                                                                                                                                                                                                                                                                                                                                     ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
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   Metazoa;
                                    (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 44, Last amnotation update)
450 3A12 (EC 1.14.14.1) (CYPIII
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   Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2112;
Pred. No. 9.
   Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D0B8902ADDF33810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                      n update)
(CYPIIIA12)
                                                                                                 503
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                                       (P450-PBD-1)
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   Euteleostomi;
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                                                                                                                                   MVPIIAQYGDVLVRNLLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
OKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                       ENTKKLLKFOFLDPFFFFSILLFPFLTPVFEILNIWLFPKKVTDFFRKSVERMKESRLKDK
                                                  ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                    MFPIIGQYGDVLVNNLRKEAEKGKAINLKDVFGAYSMDVITSTSFGVNIDSLNHPQDPFV
                                                                                                                                                                                     YGTYTHGIFRKLGIPGPTPLPFVGTALGYRNGFYVFDMKCFSKYGRMWGFYDGRQPVLAI
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Mammalia; Eutheri
NCBI_TaxID=9615;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the IIA gene subfamily.",

Biochim. Biophys. Acta 1088;319-322(1991).

Biochim. Biophys. Acta 1088;319-322(1991).

IFUNCTION: Cytochromes P450 are a group of heme-thiolate monoxygenases. In liver microsomes, this enzyme is involved NADPH-dependent electron transport pathway. It oxidizes a va of structurally unrelated compounds, including steroids, fat acids, and xemobiotics.

CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + Oxidized flavoprotein + H(2)O.

INDUCTION: P450 can be induced to high levels in liver and compounds. The statement of the property of the process of the property of the property of the process of the property o
                                                                                                                                                                                                                                                   InterPro; IPR001128; Cytochrome P450.
InterPro; IPR008072; EP450 CYP3A.
InterPro; IPR008072; EP450T.
Pfam; PP00067; p450; 1.
PRINTS; PR00463; EP450I.
PRINTS; PR00463; EP450IICYP3A.
PRINTS; PR00469; EP450.
PRINTS; PR00385; P450.
PROSITE; PS00386; CYTOCHROME P450; 1.
Electron transport, Endoplasmic reticulum; Heme; Membrane; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P14779; JJPZ.
GO; GO:0005524; C:membrane fraction; ISS.
GO; GO:0004497; F:monooxygenase activity;
GO; GO:0006805; P:xenobiotic metabolism; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMEL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ciaccio P.J., Graves P.E., Both Halpert J.R.; CDNA and deduced amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Beagle; TISSUE=Liver; MEDLINE=91159488; PubMed=2001406; DOI=10.1016/0167-4781(91)90072-T; Ciaccio P.J., Graves P.E., Bourque D.P., Glinsmann-Gibson B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and carcinogens.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
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                                                                                                                                                                                                                                  Monooxygenase;
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YGTHSHGLFKKLGIPGPTPLPPLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
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Conservative 59
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57721 MW;
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                                                                          Score 2077; D
Pred. No. 3.5e
55; Mismatches
                                                                                                                                                                                   Iron (heme axial ligand)
; 52171D03F9BD5D87 CRC64;
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GO; GO:0004497; F:monooxygenase activity; I:
GO; GO:0006405; P:xenobiotic metabolism; ISS.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP450I.
InterPro; IPR008072; EP450_CYP3A.
Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP450I.
PRINTS; PR00385; EP450I.
PRINTS; PR00385; P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser D.J., Feyereisen R., Harlow G.R., Halpert J.R.; Submitted (SEP-2002) to the EMBL/GenBank/DDJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; AF547269; AAN47145.1; -.
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00086; CYTOCHROME P450; UNKNOWN Heme; Monooxygenase; Oxidoreductase. SEQUENCE 503 AA; 57726 MW; AFBC66002CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Praser D.J., Feyereisen R., Harlow G.R., Halpert J.R.;
"ISOLATION, heterologous expression and functional characterization
a novel cytochrome P450 3A enzyme from a canine liver cDNA library.'
J. Pharmacol. Exp. Ther. 283:1425-1432(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
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                       MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
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MFPIIGQYGDVLVNNLRKEAEKGKAINLKDVFGAYSMDVITSISFGVNIDSLNHPQDPFV
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                                                                                                                                                                                                                                                                             Conservative
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77.9%;
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Pred. No. 2.2e-13
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CD39 RAT

CD39 RAT

CD39 RAT

CD39 RAT

CD3155; 064557; 064631;

DT 01-0CT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 34, Last annotation update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DT 01-NOV-1997 (Rel. 44, Last annotation update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DT 01-NOV-1997 (Rel. 44, Last annotation update)

DT 01-NOV-1997 (Rel. 44, Last annotation update)

DT 01-NOV-1997 (Rel. 44, Last annotation update)

CC NCBI_TaxID=10116;

RN 150UENCE FROM N.A.

RC STRAIN-Sprague-Dawley;

RI Mahnke A., Strotkamp D., Roos P.H., Hanstein W.G.

RR "Expression and inducibility of cytochrome P450;

RR "Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang H., Kawashima H., Strobel H.W.;
"cDNA cloning of a novel CYP3A from rat brain.";
Biochem. Biophys. Res. Commun. 221:157-162(1996).
-I- FUNCTION: This isozyme seems to be implicated in olfaction. A in the demethylation of erythromycin as well as benzphetamine
-I- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)O.
-I- SUBCELIQUAR LOCATION: Membrane-bound. Endoplasmic reticulum.
-I- TISSUE SPECIFICITY: Mainly expressed in olfactory epithelium.
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-corsend an email to license@isb-sib.ch).
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MEDLINE-97144501; PubMed-8990268; DOI=10.1006/abbi.1996.9752;
Mahnke A., Strotkamp D., Roos P.H., Hanstein W.G., Chabot G.G
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Wang H., Kawashima H., Strobel H.W.;
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PF4sm; PP00667; P450; 1.

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PRINTS; PR01689; EP450I.

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PROSITE; PS00086; CYTOCHROME P450; 1.

Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;

MY MODOOXYGENASe; Olfaction; Oxidoreductase.

PT CONFLICT 457 457 F -> V (in Ref. 2).

SEQUENCE 503 AA; 57811 MW; 9BBB13E690675EB4 CRC64;
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## ALIGNMENTS

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482. .485
/note= "Synthetic His tag" Location/Qualifiers protein; 485 B PA, Jhoti H, region' Kirton cytostatic; cancer; His tag.

Obtaining a representation of the 3-D structure of cytochrome P450 3A4 crystals, by providing data of structure factors used to generate electron density map of crystal structure and constructing electron density map of obtained data.

The invention relates to a novel method for obtaining a representation of the 3-dimensional structure of a crystal of cytochrome P450 (CYP)3A4 which involves providing the data of structural factors and phases used

Claim 64; SEQ ID NO 2; 357pp; English

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Best Local Simi
Matches 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to generate an electron density map of 3A4 crystal structures as given in specification and constructing an electron density map of the structural factors and phases. The method of the invention has cytostatic applications and may be useful for obtaining a representation of the 3-dimensional structure of a crystal of CYB3A4, where the crystal structure is useful in modelling the interaction of a compound with the protein and in drug design. Such information may be utilised on order to generate a composition to treat cancer. The current sequence is that of the human CYB3A4 N-terminal truncated protein of the invention which has a synthetic N-terminal region in place of the hydrophobic transmembrane domain in order to aid Escherichia coli expression and solubility, in addition to a C-terminal His tag which facilitates purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                          Homo sapiens.
                                                                                  cytochrome P450;
                                                                                                             Human
                                                                                                                                          06-MAY-2004
                                                                                                                                                                                              ADJ87521
                  WO2003102192-A1
                                            Unidentified.
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                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                           AHHHH
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                                                                                                             P450 3A4 protein
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Query Match
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Matches 484;
                                                                                         The invention relates to a method of purifying a cytochrome P450 by expressing in a host cell culture a cytochrome P450 molecule, recovering the cells from the culture and suspending the cells in a salt buffer having a conductivity of 12-110 mS/cm, lysing the cells and removing cell debris to provide a high-salt lysate, adding to the lysate a detergent to provide a high-salt-detergent lysate, and recovering the P450 from the lysate. Methods of preparing and purifying cytochrome P450 proceins are useful for X-ray crystallographic studies and crystallographic screening of small molecules bound to P450, or for NMR studies and high-throughput screening methods to discover drugs or analyze the interaction of drugs with P450 molecules. This sequence corresponds to the human cytochrome P450 3A4.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                               Purifying a cytochrome P450, for NWR studies and high-throughput screening methods to discover drugs, comprises suspending cells expressing P450 molecule in a salt buffer, lysing the cells and a high-salt-detergent lysate.
                                                                Sequence 485
                                                                                                                                                                                                                                                                                                     Claim 12;
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DB; ADJ87520.
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                  Similarity
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                                        IGMRFALMIMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG
                                                      IGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG
                                                                                              INGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a cytochrome P450 protein (I) in which CYP3A43 exon. 1s joined to sets of CYP3A4 or CYP3A5 exons, as well as subfragments, variants and multiples of (I) having essentially the same characteristics. (I) Is useful as a medicament, and for evaluating drug metabolism, in drug design, and drug screening, and in tests for adjusting the dose of drugs. This is the amino acid sequence of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating metabolism, in drug design and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 503 AA;
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drug metabolism;
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11-JUN-2001;
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OKHRVDELQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
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                                                                                      ENTKKLLREDELDPEFLSITVEPFLIPILEVLNICVFPREVTNELRKSVKRMKESRLEDT
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100.0%; Pred. No. 5.4e-226;
Live 0; Mismatches 0;
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                                                      This invention relates to a transgenic non-human animal which may be used CC for assessing the behaviour and/or metabolism of a drug in another animal CC and which expresses a foreign polypeptide associated with drug behaviour and/or metabolism. The invention also comprises a nucleic acid construct CC for use in producing the above transgenic non-human animal and a method of assessing the metabolism and/or behavior of a drug in an animal of interest, comprising administering a test agent to the transgenic animal and conducting analytical tests to determine drug metabolism and/or behaviour. The transgenic animal is useful in studying drug metabolism and/or behaviour in other animals. The nucleic acid construct is useful in producing the above transgenic animal and the methods are used for producing, breeding and using transgenic animals for pharmacological (e.g. pharmacokinetic or pharmacodynamic assays) and/or toxicological studies. Nucleic acid sequences used within the invention are serum albumin, alpha-acidic glycoprotein; cytochrome p450 (CYP); uridine CC diphosphoglucuronosyl transferase (UCT); multidrug resistance proteins and (MRP's). The present sequence represents a protein sequence used to create a transgenic animal within the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New transgenic non-human animal expressing a foreign polypeptide associated with drug behavior and/or metabolism, useful for studying the behavior and/or metabolism of a drug in other animals.
   Sequence 503
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New protein array, useful for determining the phenotype of a naturally occurring variant of a DNA sequence of interest, comprises a surface up which at least two protein moieties are deposited.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a protein array comprising a surface upon which at least two protein moieties are deposited at spatially defined concations, where the protein moieties are naturally occurring variants of concations, where the protein moieties are naturally occurring variants of concations, where the protein moieties for molecules that interact with one or more proteins; and (3) simultaneously determining the relative properties of members of a set of protein moieties. The protein array can be used for determining the phenotype of a naturally occurring variant of a DNA sequence of interest. The protein array is useful for drug cdiscovery, pharmacogenomics and diagnostics. The protein array allows the parallel analysis of closely related proteins with a sensitivity that is at least comparable to existing methods, if not better, with small comparative functional analysis manner not previously possible. ACF06000 to ACF06056 and ABR81975 to ABR82026 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Sim
Matches 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 503 AA;
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                MRFALMMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  TDPDMIKTVLVKECYSVFTNRRPFGFVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
                                                                                   GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG
                                                                                                                                                       PDVQQXLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
                                                                                                                                                                                                                           QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                                                                                                                                                                                                                                                        ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                                                                                                                                                                                                                                                                                                                                              TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
                                                                  GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG
                                                                                                                                      PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
                                                                                                                                                                                                      QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 11B; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.4%; Score 2501; DB 6; 100.0%; Pred. No. 5.4e-226;
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RESULT 6
ADL18578
ID ADL1
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AC ADL1
XX
DT 06-M
XX
DE Huma
XX
DE Huma
XX
CHUM
XX
SHOMC
XX
OS Homc
                   drug metabolic activity; CYP3A4; single nucleotide polymorphism.
                                                                       06-MAY-2004
                                                                                                             ADL18578 standard;
                                                  Human
                                                wild-type cytochrome
                                                                      (first entry)
                                                                                                             protein;
                                                  P450
                                                                                                              ₿
                                                 CYP3A4
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human; wild-type; cytochrome P450; SNP;

protein.

Homo sapiens

5

423

MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA

481

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for testing the drug metabolic activity of CYP3A4 by detecting the CYP3A4 gene polymorphisms in which the drug metabolic activity of CYP3A4 is reduced. The method of the invention may be useful for testing the possibility of a side effect resulting from a drug metabolised by CYP3A4 in a subject. The current sequence is that of the human wild-type cytochrome P450 CYP3A4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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hydroxylase
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N-PSDB; ADL18577.
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                                                                                                                                                                                                                                                                                                                                                                                                                     MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                                                                                                                                                          QKHRVDF1QLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                                                                                                                                                                                                                                                                                                     ENTKKLLRFDFLDFFFLSITVFPFLIFILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the drug metabolic activity of CYP3A4 such as testosterone ase activity by detecting the CYP3A4 gene polymorphisms in metabolic activity of CYP3A4 is reduced.
                         GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
                                                                                                                                                                                                                                                                                                                                                                                         MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKXXXDNIDPXIYTPFGSGPRNCIG
                                                                                                                            PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
                                                                                                                                                                                           QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
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                                                                                                PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
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nucleotide polymorphism (SNP) in coding DNA"
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100.0%; Pred. No. 5.4e-226;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 503;
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밁 ક 밁 ð 뭐 8 밁 δ 문 Ś 밁 δ 밁

385

444

Query Match 98.4%; Score 2501; DB 8; Best Local Similarity 100.0%; Pred. No. 5.4e-226; Matches 479; Conservative 0; Mismatches 0;

Length 503;

Indels

0;

Gaps

0

Sequence

503

B

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RESULT 7
ADL18672
ID ADL1
CC having spatially defined locations where at each location there are complex at least two protein moieties capable of forming a complex. CC where the complex is transiently formed and where the protein moieties CC act sequentially on a substrate of interest and are derived from one or more drug metabolising enzymes (DMEs). Also described: (1) a method of CC making a protein array, (2) an array made by the method of (1); (3) a CC method of screening a set of protein moieties for molecules which CC interact with one or more proteins; (4) a method of simultaneously CC determining the relative properties of members of a set of protein CC moieties; and (5) a method of expressing and purifying a DME. The protein CC array is useful in examining gender differences in drug metabolism, CC ethnicity-related differences in drug metabolism and toxicity between two creatabolites, in defining and quantifying metabolic pathways for small CC molecules, in screening of compounds that binds and inhibits individual CC DMEs and in analysing induction of p450 expression by one or more CC compounds of interest and the effects of mutation on the activity of a CC DME of interest and the effects of mutation on the activity of a compounds of interest and the effects of mutation of the present CC invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein array comprising a surface having spatially defined locations containing drug metabolizing enzymes, examining gender and ethnicity-related differences in drug metabolism or cytotoxicity of drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-2002; 2002US-0410815P
05-DEC-2002; 2002US-00313963
05-DEC-2002; 2002WO-GB005499
                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a protein array comprising a surface
                                                                                                                                                                                                                                                                                                                                                                                                                                Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein array; protein moiety; drug metabolising enzyme; DMB; drug metabolism; drug toxicity; cytotoxicity; drug metabolite; metabolic pathway; human; cytochrome; enzyme; P450.
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DB; ADL18671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                3B;
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                                                                                                                                                                                                                                                                                                                                                                                                                               English
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                         Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; spared nerve injury; SNI; Chung.
            New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                              WPI; 2003-268312/26 GENBANK; A29815.
                                                                                                                                                                                                                                                         Homo sapiens.
Unidentified.
                                                                                                                                                                                                                                                                                                                                        Human Protein A29815, SEQ ID NO 14079
                                                                                                                                                                                                                                                                                                                                                                02-DEC-2004
29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                         ADD48378 standard;
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                                                                                                                                                                                      14-AUG-2002; 2002WO-US025765
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Example 1; Page; 1017pp; English.

XX

The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates to the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating compound that regulates the cc polynucleotides, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the polypeptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more compound that properties or their antibodies. The polynucleotide or the compound that composition comprising a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene compound that properties of the polynucleotide or the compound that the properties of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 502 AA;
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Query Match
Best Local Similarity
Matches 478; Conserv 384 363 324 303 264 243 204 183 144 84 63 24 3 YGTHSHGLEKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV MRFALMMKLALIRVLQNFSFKFCKETQIFLKLSLGGLLQFEKFVVLKVESRDGTVSGA GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG ENTKKLLRFDFLDFFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT TDPDMIKTVLYKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN OKHRVDFI QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI Conservative LQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 98.1%; Score 2494; DB 7; Pred. No. 2.5e-225; 0; Mismatches 1; Length Indels 502; ٥, Gaps 481 122 83 383 362 182 143 443 323 302 263 242 203

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RESULT 9 AAR772363 ID AAR72363 standard; protein; XX

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Best Local (
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                    The amino acid sequence of the human cytochrome P450 species 3A4. The CDNA was amplified by PCR using the primers AAQ87743-6. The product was cloned into the yeast expression vectors pAAH50 or pAHRR to produce the vectors p3A4 for the expression of the cytochrome P450 alone or p3A4R for co-expression with the yeast NADH-P450 reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species 1A2 (AAQ87714), 2C9 (AAQ87715), 2E1 (AAQ87716), or 3A4, or their auxillary species and variants (AAQ87718-32), and yeast NADPH-P450 reductase, either as a fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound, or its metabolite, will be converted into a carcinogenic or mutagenic form through metabolism in the liver. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-1993;
21-JUL-1993;
30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evaluation of safety of a chemical cpd. - expressing human cytochrome p450 and a year
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-116991/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytochrome P450; amplification; PCR; yeast NADPH-P450 reductase; safety; fusion carcinogen; mutagen; liver metabolism.
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14-NOV-1995
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205
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                                                                                                                                                                                                                                                                     503
             ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                   MVPIIAQYGDVLVRNLRR&AETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                                      TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLS
                                                                                                                      TDPDMIKTVLYKBCYSVFTNRRPFGFVGFMKSAISIAEDEEWKRLRSLLSDTFTSGKLKE
                                                                                                                                                        YGTHSHGLFKKLGI PGPTPLPFLGNILSYHKGFCMFDMECHKXYGKVMGFYDGQQPYLAI
                                                                                                                                                                                    YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
                                                MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
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(first entry)
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93JP-00180246.
93JP-00208279.
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                                                                                                                                                                                                               Score 2494; I
Pred. No. 2.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pd. - using recombinant yeast
a yeast NADPH-P450 reductase.
                                                                                                                                                                                                                           .5e-225;
                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko
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63 25 w

TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE

YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMBCHKKYGKVWGFYDGQQPVLAI

Matches

478;

Conservative

Local

Similarity

.5e-225; ₽B

Length 503; Indels

0

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62

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RESULT 10
AAR81464
ID AAR81464
ID AAR81164
AC AAR81
AC AAR81
XX AAR81
AC AA
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                                                            Query Match
                                                                                                                                                                    The present sequence is the human derived cytochrome (HDC) P4503A4, which was obtd. from a commercial cDNA library. Yeast were transfected with an expression vector contg, the HDC cDNA, cultured and then disrupted to give a microsomal fraction. The HDC was purified from the fraction, and used to immunise and sensitise a mammal. Blood was drawn from the mammal, and an anti-HDC antibody isolated. The antibody obtd. recognises HDC P4503A4, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC P450 spp
                                                                                                                   Sequence 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody recognising human derived cytochrome P4502A4 - detection of cytochrome P450 species in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-136338/14
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 10-12; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRFALMINKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA
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30-JUL-1993;
17-JUN-1994;
This is the amino acid sequence of the human cytochrome P450 molecular species 3A4 protein. The corresp. gene was amplified from a human liver derived cDNA library as 2 fragments of 0.6 and 0.9 kb using primers AAT26933-6. The prod. was cloned into the yeast expression vector pAAH5N to generate plasmid p3A4 for prodn. of the cytochrome only or into the vector pAHRR to generate the plasmid p3A4R for co-prodn. with the yeast NADPH-P450 reductase. The sequence is placed under control of the yeast NADPH-P450 reductase. The sequence is placed under control of the yeast NADPH gene promoter and terminator. The vectors are used in a method for
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93JP-00208279.
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DT 17-JU
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Best Local Sim:
Matches 478;
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                                                                                                                                                                                                         CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism; CYP3A4 substrate; drug-drug interaction identification; toxin exposure; genetic linkage detection; phenotypic variation.
                                                                                                                                              WO9913106-A1
                                                                                                                                                                                                                                                                           Human CYP3A4
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                                                                                                               18-MAR-1999
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Antagonist of cell cycle progression
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Pred. No. 2.5e-225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the polypeptide, capable of affecting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cell cycle progression genes and proteins for modulating progression in cells, for preventing, treating or diagnosing proliferative diseases (e.g. cancer) or for identifying modulations or meiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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06-MAY-2003; 2003US-0468402P
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                                                   PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
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Pred. No. 2.5e
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RESULT 14
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                                                                                                                                                                     dynamics docking of one or more substrates on multi-specific enzymes.

Specifically, it refers to determining the three-dimensional structure of active sites that are flexible and can adapt to different substrates i.e. multispecific enzymes such as cytochrome P450. The present invention describes identifying common structural blocks (CSBs) among members of the family, aligning primary amino acid sequences, aligning the protein as compared on the first alignment to obtain a second alignment, defining 3D structure of protein CSBs, defining global constraints and selecting rotamers, in order to determine the family of 3D model protein structures and optimise models by dihedral angles. Accordingly, the method can be used for screening, designing or identifying natural, unnatural or substrate analogues, as well as inhibitors, activators or modulators of the multispecific enzyme in question. In addition, it can determine the effect of a first substrate on a second substrate, which can then be applied to pharmaceutical products. Purthermore, the method can be used to determine the exidative modification of the substrate according to its
                                   proximity to a haem molecule, for performing dynamic docking of the metabolite either in the absence or presence of a second substrate in the computed simulation and to compare the energy of the bound metabolite relative to the energy of its parent substrate bound, in order to determine if the exit of the given metabolite from the enzyme is favoured or not. This polypeptide sequence is a protein from the cytochrome P450 family of enzymes, given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Designing 3 dimensional (3D) protein model, by identifying common structural blocks (CSBs) among family members, aligning sequence, defining 3D structure of CSBs, global constraints, selecting rotamers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel method for performing restrained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining, optimizing 3D structures.
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CNRS CENT NAT RECH SCI.
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Query Match Best Local Similarity

97.0%;

Score 2466; DB 8; Pred. No. 1.1e-222;

Length 502;

This invention relates to a novel method for performing restrained

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Matches
                                      Designing 3 dimensional (3D) protein model, by identifying common structural blocks (CSBs) among family members, aligning sequence, defining 3D structure of CSBs, global constraints, selecting rotar determining, optimizing 3D structures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dynamics docking; cytochrome protein coordinate data; com
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    Disclosure; SEQ
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CNRS CENT NAT RECH SCI.
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    NO 10;
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CC dynamics docking of one or more substrates on multi-specific enzymes.
CC Specifically, it refers to determining the three-dimensional structure of continue site of the tare flexible and can adapt to different substrates i.e. compared on the first alignment to obtain a second alignment, defining common structural blocks (CSBs) among members of the family, aligning primary amino acid sequences, aligning the protein CC as compared on the first alignment to obtain a second alignment, defining continues, in order to determine the family of 3D model protein structures and optimise models by dihedral angles. Accordingly, the method can be used for screening, designing or identifying natural, unnatural or cubstrate analogues, as well as inhibitors, activators or modulators of the multispecific enzyme in question. In addition, it can determine the continues of the determine the oxidative modification of the substrate according to its parlied to pharmaceutical products. Furthermore, the method can be used to determine the oxidative modification of the substrate according to its provinity to a haem molecule, for performing dynamic docking of the computed simulation and to compare the energy of the bound metabolite computed simulation and to compare the energy of the bound metabolite computed simulation and to compare the energy of the bound metabolite continues if the exit of the given metabolite from the cytochrome p450 can be used to family of enzymes, given in an exemplification of the invention.

ពួកព័ត្ធស្ថិត្តស្ថិត្តស្ថិត្តស្ថិត្តស្ថិត្តស្ថិត្តស្ថិត្ត Matches 470; Conservative Query Match Best Local : Sequence 503 AA; Local Similarity 96.4%; 97.9%; Score 2449.5; DB 8; Length 503; Pred. No. 3.8e-221; 4; Mismatches 5; Indels 1; Gaps

밁 S 밁 á 밁 Ś 문 5 맑 S 밁 Ś 밁 384 362 324 422 302 264 243 204 183 144 444 123 84 63 24 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA NGMF1PKGWVVM1PSYALHRDPKYWTEPEKFLPERFSKKNKDN1DPY1YTPFGSGPRNC1 HPDVQQXLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI MVPIIAQYGDVLVRNLRREAETGKFVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDFFV 182 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242 MVPIIAQXGDVLVRNLRRERETGKPVTLKDVFGAYSMDVITSSSFGVNVDSLNNPQDPLV 203 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI ENTKKLLREDELDPEFLSITVEPFLIPILEVLNICVEPREVINFLRKAVKRMKESRLEDT TDPDMIKLVLVKECYSVFTNREPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 143 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 83 481 443 421 383 361 263

Search completed: July 8, 2005, 14:26:00 Job time: 171 secs

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Maximum DB seq length: 200000000
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Maximum Match 100%
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     2449.5
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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2542
     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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     BB
     A29815
A298168
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XX0062
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
520	520.5	528.5	529	530.5	543.5	556.5	587	588.5	590.5	591.5	594	595.5	599	602.5	620.5
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475	501	544	494	513	496	515	520	522	510	518	520	503	517	509	519
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A88414	T19766	T27750	JC5320	JC7120	S41192	T24781	T24780	T19762	T19763	T24779	T24778	JC5321	T20907	T24785	T24784
4	hypothetical prote	hypothetical prote	cytochrome P450 mo	cytochrome P450 en	cytochrome P450 4D	<ul> <li>hypothetical prote</li> </ul>	hypothetical prote	cytochrome P450 mo	hypothetical prote	hypothetical prote	hypothetical prote				

## ALIGNMENTS

Cibble 130 Sept. 1938 Secquiron. Cibble 130 Sept. 1938 Secquiron. Cibble 130 Sept. 1938 Sept. 181800; AZSSI7; AZSI9; PX0012; S03851 Cibble 130 Sept. 1938 Sept. 181800; AZSSI7; AZSI9; PX0012; S03851 Cibble 130 Sept. 1938 Sept. 1938 Sept. 181800; AZSSI7; AZSI9; PX0012; S03851 Cibble 130 Sept. 1938 Sept. 1938 Sept. 181800; MCD12; S03851 Cibble 130 Sept. 181800; AZSSI5; MUID:88185781; PMID:3867210 A; Accession: AZSSI5; MUID:89108438; PMID:3867210 A; Accession: AZSSI5; MUID:89108438; PMID:2863251 A; Accession: S16900 A; Title: The human cytochrome P450 CYP3 locus: assignment to chromosome 7q22-qtex. A; Accession: S16900 A; Cibble 14 Type: mENA A; ARSSIDE 18180; MUID:89108438; PMID:2863251 A; Accession: S16900 A; Cibble 18180; ACC; Stevenson, K; Wolf, Ca.R. A; Accession: S16900 A; Cibble 18180; ACC; Stevenson, K; Wolf, Ca.R. A; Accession: S16900 A; Cibble 18180; ACC; Stevenson, K; Wolf, Ca.R. A; Accession: AZSSI7; MUID:89108438; PMID:2863251 A; Accession: AZSSI7; MUID:87041402; PMID:363044.1; PID:935911 A; Accession: AZSSI7; MUID:87041402; PMID:3464943 A; Accession: AZSSI7; MUID:87041402; PMID:3464943 A; Accession: AZSSI7; MUID:87041402; PMID:3464943 A; Accession: AZSSI7; MUID:8903163; PMID:3464943 A; Accession: AZSSI7; MUID:8903163; PMID:3463943 A; Accession: AZSSI7; MUID:8903163; PMID:346396 A; ACCESSION: AZSSI7; MUID:8903163; PMID:346396	RESULT 1 A29815 cytochrome P450 3A4 nifedipine oxidase (EC 1.14.14) - human N;Alternate names: cytochrome P450(PCN1); cytochrome P450-HM1 C.Species: Homo saniens (man)
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RESULT 2
A29410
Cytochrome P450, glucocorticoid-inducible, hepatic - human
Cytochrome P450, glucocorticoid-inducible, hepatic - human
Cytochrome P450, glucocorticome P450 3A3; cytochrome P450 HLp
N;Alternate names: cytochrome P450 3A3; cytochrome P450 HLp
N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 09-Jul-2004
C;Date: 31-Mar-1989 #sequence of 311-S15, 1986
A;Molowa, D.T.; Schuetz, B.G.; Wrighton, S.A.; Watkins, P.B.; Kremers, P.; Mende Proc. Natl. Acad. Sci. U.S.A. 83, 5311-5315, 1986
A;Title: Complete cDNA sequence of a cytochrome P-450 inducible by glucocortico:
A;Accession: A29410
A;Accession: A29410
A;Accession: A29410;
A;Acce
                                                                                                                       A;Cross-references: UNIPROT:P05184; GB:M13785; NID:g181353; PID
R;Watkins, P.B.; Wrighton, S.A.; Maurel, P.; Schuetz, E.G.; Men
Proc. Natl. Acad. Sci. U.S.A. 82, 6310-6314, 1985
A;Title: Identification of an inducible form of cytochrome P-45
A;Reference number: A25170; MUID:85298342; PMID:3898085
A;Accession: A25170
A;Accession: A25170
A;Molecule type: protein
A;Residues: 2-21 <WAT'>
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 ho
C;Keywords: chromoprotein; electron transfer; heme; iron; liver
F;303-465/Domain: Cytochrome P450 homology <P45>
F;443/Binding site: heme iron (Cys) (axial ligand) #status pred
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                                                                                                                       Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology keywords: chromoprotein; electron transfer; heme; iron; liver; meta skeywords: chromoprotein; electron transfer; heme; iron; liver; meta 303-465/Domalin: cytochrome P450 homology cP45> cytochrome P450 homology cP45>
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                     Score 2449.5; DB 2;
Pred. No. 2.6e-175;
4; Mismatches 5;
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                                                                                                                                                           NGMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI
                                                                                                                                                                              NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI
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P450-MK2
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RESULT 3
Signife
Signife oxidase (RC 1.14.14.-) cytochrome P450 3A8 - crab-eating macaque nifedipline oxidase (RC 1.14.14.-) cytochrome P450 MKnf2; cytochrome P450-MK2
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Catcession: Signife; S04509; S36875
R;Komori, M.; Kikuchi, O.; Sakuma, T.; Funaki, J.; Kitada, M.; Kamataki, T.
Biochim. Biophys. Acta 1171, 141-146, 1992
A;Title: Molecular cloning of monkey liver cytochrome P-450 cDNAs: similarity of the A;Reference number: S28166; MUID:93129612; PMID:1282830
A;Accession: S28168
A;Status: not compared with conceptual translation
A;Kolceule type: mRNA
A;Residues: 1-503 KOMS
A;Cross-references: UNIPROT:B33268; GB:S53047; NID:9263692; PIDN:AAB24952.1; PID:926:A;Cross-references: UNIPROT:B33268; GB:S53047; NID:9263692; PIDN:AAB24952.1; PID:926:A;Cross-reference number: S04509; MUID:B3268; GB:S53047; MID:9263692; PIDN:AAB24952.1; PID:926:A;Cross-reference number: S04509; MUID:89287352; PMID:2500151
A;Reference number: S04509; MUID:89287352; PMID:2500151
A;Recession: S04509; MUID:89287352; PMID:2500151
A;Cross-reference number: S36874; MUID:89287352; PMID:2500151
A;Cross-reference number: S36874; MUID:93384294; PMID:8373178
A;Cross-reference number: S3 93.3**%**; 93.9**%**; 2372; DB 2; No. 1.6e-169; PID:g263693 cytochrome crab-eat the metallc pr

Score Pred.

J.

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Cytochrome P450 3A7 - human
N.Alternate names: cytochrome P450 3A3; cytochrome P450 HFL33; cytochrome N. Alternate names: cytochrome P450 3A3; cytochrome P450 HFL33; cytochrome N. Cipacis: Homo Sapiens (man)
C;Spacis: Homo Sapiens (man)
C;Accession: X0062; PX0014; S04983; S02152
R;Komori, M.; Nishio, K.; Ohi, H.; Kitada, M.; Kamataki, T.
J. Biochem. 105, 161-163, 1989
A;Title: Molecular cloning and sequence analysis of cDNA containing the enterprise of the c
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A34101
cytochrome P450 3A5 - human
cytochrome P450 3A5 - human
N;Alternate names: cytochrome P450 HLp2
N;Contains: oxidoreductase (EC 1....)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A34101; S06491; T52302
R;Aoyama, T.; Yamano, S.; Waxman, D.J.; Lapenson, D.P.; Meyer, U.A.; Fischer, V.; Tyn
J. Biol. Chem. 264, 10388-10395, 1989
A;Title: Cytochrome P-450 hPCN3, a novel cytochrome P-450 IIIA gene product that is c
DNA-expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and cyclosporin
DNA-expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and cyclosporin
Nacference number: A34101; MUID:89278095; PMID:2732228
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A; Residues: 1-11, 'X'
C; Genetics:
A; Gene: GDB: CYP3A7
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A;Cross-references: GDB:134409
A;Cross-references: GDB:134409
A;Map position: 7922.1-7922.1
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; l
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; l
F;302-464/Domain: cytochrome P450 homology <P45>
F;302-464/Domain: cytochrome P450 homology <P45>
                                                                              A;Molecule type: mRNA
A;Residues: 1-502 <AOY>
A;Residues: 1-502 <AOY>
A;Cross-references: UNIPROT:P20815; GB:J04813; NID:g181345; PIDN:AAA02993.1;
R;Schuetz, J.D.; Molowa, D.T.; Guzelian, P.S.
A;Ch. Biochem. Biophys. 274, 355-365, 1989
A;Title: Characterization of a cDNA encoding a new member of the glucocortico
A;Reference number: S06491; MUID:90025114; PMID:2802615
A;Accession: S06491
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-304,'P',306-317,'F',319-323,'D',325-376,'G',378-502
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Pred. No. 3.9e
27; Mismatches
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3.9e-159;
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R;Jounaidi, Y.; Guzelian, P.S.; Maurel, P.; Vilarem, M.J.
Biochem. Biophys. Res. Commun. 205, 1741-1747, 1994
A;Title: Sequence of the 5'-flanking region of CYP3A5: comparative analysis wi
A;Reference number: 152302; MUID:95110318; PMID:7811260
A;Accession: 152302
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-24 <RES>
A;Cross-references: GB:S74699; NID:9786472; PIDN:AAD14157.1; PID:94261857
C;Genetics:
A;Gene: GDB:CYP3A5
A;Gene: GDB:CYP3A5
A;Gene: GDB:CYP3A5
A;Gene: GDB:CYP3A5
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mono
F;302-463/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
A;Cross-references: C;Genetics:
A;Gene: CYP3A
C;Superfamily: human
                                                                                             Biochim. Biophys. Acta 1088, 319-322, 1991
A;Ticle: cDNA and deduced amino acid sequences of A;Reference number: $14275; MUID:91159488; PMID:20 A;Accession: $14275
A;Residues: 1-503 <CIA>A;Residues: 1-503 <CIA>A;Cross-reference
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Pred. No. 2.3e-
37; Mismatches
                                                                                         EMBL: X54915; NID: g909;
      CYP3A5;
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PMID:2001406
      cytochrome
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TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE

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C;Accession: 04702
R;Wang, H.; Kawashima, H.; Strobel, H.W.
Biochem. Biophys. Res. Commun. 221, 157-162, 1996
A;Title: cDNA cloning of a novel CYP3A from rat brain.
A;Reference number: JC4702; MUID:96220175; PMID:8660328
A;Accession: JC4702; MUID:96220175; PMID:8660328
A;Accession: JC4702
A;Accession: JC4702; MUID:96220175; PMID:8660328
A;Cross-references: UNIPROT:P51538; GB:U46118; NID:g1276917; PIDN:AAC5258; C;Comment: This protein is involved in imipramine metabolism. It catalyzes C;Genetics:
A;Genetics:
A;Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome P450 3A9 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996
C:Accession: JC4702
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Pred. No. 1.8e-147;
5; Mismatches 42;
                                                                                                         Score 2003; DB 2;
Pred. No. 6.2e-142;
1; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                      GB:U46118; NID:g1276917; PIDN:AAC52582.1; PID:g12769 in imipramine metabolism. It catalyzes the demethyla
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RESULT 8
A34236
A34236
Cytochrome P450 3A6 (version 2) - rabbit
N;Alternate names: cytochrome P450 3C
N;Contains: oxidoreductase (BC 1.-.-)
C;species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C;Accession: A34236
R;Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Grii
J. Biol. Chem. 264, 16222-16228, 1989
A;Title: Regulation of the rabbit cytochrome P-450 3c gene. Age.
A;Reference number: A34236; MUID:89380226; PMID:2777787
A;Accession: A34236
A;Molecule type: mRNA
A;Residues: 1-501 <POT>
A;Gene: CYP3A6
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 hor C;Keywords: chromoprotein; electron transfer; heme; iron; metall F;300-467/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predi
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| OKHRVDELQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH
                                                                                             TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKB
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                                                                                                                                                                                                                                                                           78.2%;
76.0%;
                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                              Score 1989; DB 2; Length 501;
Pred. No. 6.9e-141;
4; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tukey, R.H.; Griffin, K.J.; Schwab,
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C;Superfamily: h
C;Keywords: chro
F;302-464/Domain
F;442/Binding si
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N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change |
C;Accession: S50211; S18155
R;Yanagimoto, T.; Itoh, S.; Sawada, M.; Hashimoto, H.; Kamataki, Biochim. Biophys. Acta 1201, 405-410, 1994
A;Title: Wolecular cloning and functional expression of a mouse |
A;Reference number: S50211; MUID:95101705; PMID:7803471
A;Accession: S50211
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A;Residues: 1-503 <YAN>
A;Cross-references: UNIPROT:Q64464; EMBL:X63023; NID:g50634;
C;Genetics:
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Best Local S
Matches 361
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;442/Binding site: heme iron (Cys) (axial ligand) #status predicted
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MRFALMNIKLALVRLMQNFSFKLCKETQVFLKLGKQGLLQPEKPIVLKVVSRDGIIRGA
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75.7%;
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Pred. No. 8.6e-139;
1; Mismatches 55;
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PID:g5063

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cytochrome P450 3A isoform, CYP3A43 protein - human
C;Species: Homo saptens (man)
C;Species: Homo saptens (man)
C;Accession: JC7627
C;Accession: JC7627
R;Westlind, A.; Malmebo, S.; Johansson, I.; Otter, C.; Andersson, T.B.; Ingelman-Sundber
Biochem. Biophys. Res. Commun. 281, 1349-1355, 2001
A;Title: Cloning and tissue distribution of a novel human cytochrome P450 of the CYP3A s
A;Reference number: JC7627; MUID:21139777; PMID:11243885
A;Accession: JC7627
A;Molecule type: mRNA
A;Residues: 1-503 <WES>
A;Cross-references: UNIPROT:Q9HB55; GB:AF337813
C;Gemetrics: This CYP3A43 protein has broad and overlapping substrate specificities, and a
C;Genetics: CYP3A43
A;Trrong-72/7: 55/3. 71/2. 106/3. 144/3. 174/2. 224/1. 266/3. 280/1. 342/3. 418/2. 473
A;Trrong-72/7: 55/3. 71/2. 106/3. 144/3. 174/2. 224/1. 266/3. 280/1. 342/3. 418/2. 473
A.Trrong-72/7: 55/3. 71/2. 106/3. 144/3. 174/2. 224/1. 266/3. 280/1. 342/3. 418/2. 473
A.Trrong-72/7: 55/3. 71/2. 106/3. 144/3. 174/2. 224/1. 266/3. 280/1. 342/3. 418/2. 473
A.Trrong-72/7: 55/3. 71/2. 106/3. 144/3. 174/2. 224/1. 266/3. 280/1. 342/3. 418/2. 473
A.Trrong-72/7: 55/3. 71/2. 106/3. 144/3. 174/2. 224/1. 266/3. 280/1. 342/3. 418/2. 473
A.Trrong-72/7: 418/2. 473
J. Biol. Chem. 260, 7435-7441, 1985
A;Title: Complete cDNA and protein sequence
A;Reference number: A22631; MUID:85207783; P
A;Accession: A22631
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                                                     of a pregnenolone 16-alpha-carbonitrile-ind
PMID:3838989
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submitted to the EMBL Data Library, December A, Reference number: $21697

A, Accession: $21697

A, Molecule type: mRNA
A, Residues: 1-206, 'A', 208-212, 'I', 214-231, 'V'
A, Cross-references: EMBL: X64401; NID:g56038; R; Ribeiro, V.; Lechner, M.C.
Arch. Biochem. Biophys. 293, 147-152, 1992
A, Title: Cloning and characterization of a no A, Reference number: $36137; MUID:92117688; PM
A, Accession: $36137; MUID:92117688; PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cooper, K.O.; Reik, L.M.; Jayyosi, Z.; Bandiera, S.; Kelley, M.; Ryan, Arch. Blochem. Blophys. 301, 345-554, 1993
A;Title: Regulation of two members of the steroid-inducible cytochrome P4
A;Reference number: S30378; MUID:93213168; PMID:7681660
A;Accession: S30378
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A;Accession: PX0035
A;Mocession: PX0035
A;Mocession: PX0036
A;Residues: 1-26 <ANG>
A;Experimental source: liver, Sprague-Dawle
R;Lechner, M.C.
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A; Molecule type: mRNA
A; Residues: 1-504 <GON)
A; Cross-references: UNIPROT: P04800; GB: M10161; NID: g203777; PIDN: AAA41035.1;
A; Cross-references: UNIPROT: P04800; GB: M10161; NID: g203777; PIDN: AAA41035.1;
A; Magata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
J. Biochem. 107, 718-725, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Burger, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 2145-2149, 1992
A;Title: Paradoxical transcriptional activation of rat liver to primary monolayer cultures of adult rat hepatocytes.
A;Reference number: I59218; MUID:92196074; PMID:1372436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Telhada, M.B.; Pereira, T.M.; Lechner, M.C. Arch. Biochem. Biophys. 298, 715-725, 1992
A;Title: Effect of dexamethasone and phenobarbital on run-on A;Reference number: S27107, MUID:93037516; PMID:1417000
A;Accession: S27107
                                                                                                                                                                                                                                                           A;Gene: CYP3A1, P450p

C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein;
E;303-465/Domain: cytochrome P450 homology <P455
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A;Residues: 205-206, 'A', 208-212, 'I', 214-231, 'V', 233-234
A;Cross-references: EMBL:X64401
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                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M86850; NID:g205919; PIDN:AAA41780.1; PID:g205920
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1-25 < COO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-24 <TEL>
A;Cross-references: EMBL:X62086
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A; Residues: 1-24 <BUR>
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                                                                                                                  Matches
                                                                                                                                                                              Query Match
                                                                                                                                                  Local
                                                                                                                  355;
                                                       3 YGTHSHGLFKXLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
                                                                                                                                                  Similarity
FGTRTHGLFKKQGIPGPKPLPFFGTVLNYYMGLWKFDVECHKKYGKIWGLFDGQMPLFAI
                                                                                                                      Conservative
                                                                                                                                                  76.6%; Score 1946.5; 74.0%; Pred. No. 1e-1;
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NID:g56038; |
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PMID:1731631
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PIDN:CAA45743.1;
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MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV TDTEMI KNVLVKBCFSVFTNRRDFGPVGIMGKAVSVAKDBEWKRYRALLSPTFTSGRLKE TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122

182

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RESULT 12

A29487

A29487

A29487

Cytochrome P450 3A6 (version 1) - rabbit

N;Alternate names: cytochrome P450 3c

N;Contains: oxidoreductase (EC 1.-.-)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-00;C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-00;C;Accession: A29487

R;Dalet, C.; Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maure DNA 7, 39-46, 1988

A;Title: Complete sequence of cytochrome P450 3c cDNA and presence ch;Reference number: A29487; MUID:88166352; PMID:3349903

A;Accession: A29487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P11707; GEORGES:
C;Genetics:
A;Gene:CYP3A6
C;Superfamily: human cytochrome P450 C;Superfamily: human cytochrome P450 C;Keywords: chromoprotein; electron tx F;301-462/Domain: cytochrome P450 home F;301-462/Domain: cytochrome P450 home F;440/Binding site: heme iron (Cys) (descriptions)
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A; Residues: 1-501 < DAL>
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Best Local S
Matches 359
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Keywords: chromoprotein; electron transfer; heme; iron; metalloprot;
301-462/Domain: cytochrome P450 homology <P45>
;440/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                      TQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT
                                                                                                                                                                                                                                                                       HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI
                                                                                                                               VKNVRRLLKFSFFDFLLLSITLFFFLTFIFEALHISMFFKDVMDFLKTSVEKIKDDRLKD
                                                                                                                                                                                                                       EMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPF
                                                                                                                                                                                                                                                                                                                                                                 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCM-FDMECHKKYGKVMGFYDGQQPVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLED
                                                                                                                                                                                                    EMIPITAQYGDVLVKNIRQEAEKASPSTIKETFGAYSMDVITGTSFGVNIDSIRNPQDPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGTSTHGLFKKMGIPGPTPLPFIGTILBYRKVINWDFDIECRKKYGKMWGLFDGRQPLMV
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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74.8%;
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Pred. No. 5.3e-137;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Superfamily: human cytochrome P450 cyp3a5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum;
P;303-465/Domain: cytochrome P450 homology <P45>
P;443/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Contains: oxidoreductase (EC 1.-.-.)
(;Species: Mus musculus (house mouse)
(;Date: 17-Apr-1993 #sequence revision 17-May-1996 #text_change 09-Jul
(;Accession: $22334; A60564
R;Yanagimoto, T.; Itoh, S.; Muller-Enoch, D.; Kamataki, T.
Biochim. Biophys. Acta 1130, 329-332, 1992
A;Title: Mouse liver cytochrome P-450 (P-450IIIAM1): its cDNA cloning
A;Reference number: $22334; MUID:92223116; PMID:1339292
A;Accession: $22334
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A;Residues: 1-17,'X',19-20,'X',22-24 <BOR>
C;Comment: This member of the cytochrome P450IIIA family
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A;Title: Selective inactivation of mouse liver cytochrome A;Reference number: A60564; MUID:90384441; PMID:2402224
A;Accession: A60564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
A60564
cytochrome P450 3A11 - mouse
N;Alternate names: cytochrome P450 3A-UT; cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q64459; R;Bornheim, L.M.; Correia, M.A.
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                                                        QKHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT
                                                                                                                                                                                                    EKAKKLLRFDFFDPLLFSVVLFPFLTPVYEMLNICMFPKDSIEFFKKFVDRMKESRLDSK
                                                                                                                                                                                                                       ENTKKLLRFDFLDFFFLSITVFPFLIFILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                                                                                                                                                                                                                                                                              TDPETIKNVLVKECFSVFTNRRDFGPVGIMSKAISISKDDEWKRYRALLSPTFTSGKLKE
                                                                                                                                                                                                                                                                                                                                                                   TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
                                                                                                                                                                                                                                                                                                                                                                                                                    YGTRKHELFKKQGIPGPKPLPELGTVLNYYKGLMKFDMECYKKYGKTWGLFDGQTPLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                          YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMPDMECHKKYGKVWGFYDGQQPVLAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKONIDPYIYTPFGSGPRNCI 421
                                                                                                                             QKHRVDFLQLMMNSHNNSKDKVSHKALSDMEITAQSIIFIFAGYETTSSTLSFTLHSLAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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73.1%; Pred. No. 6.9e-137;
tive 64; Mismatches 64; Indels
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-27, 'X', 29, 'X', 31-33 < NA2>
A; Residues: 1-27, 'X', 29, 'X', 31-33 < NA2>
A; Residues: 1-27, 'X', 29, 'X', 31-33 < NA2>
A; Residues: 1-27, 'X', 29, 'X', 31-33 < NA2>
A; Residues: 1-27, 'X', 29, 'X', 31-33 < NA2>
A; Residues: No.; Reik, L.M.; Jayyosi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, R
Arch. Biochem. Biophys. 301, 345-354, 1993
A; Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3
A; Reference number: S30378; MUID:93213168; PMID:7681660
A; Reference number: S30378; MUID:93213168; PMID:7681660
A; Rocession: S30379
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-25 < CCOO>
C; Genetics:
A; Genetics:
A
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A;Description: Structure of a gene and cDNA of a major constitutive form of A;Reference number: $46938
A;Reference number: $46938
A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-428,'D','430-444,'G','446-504 cMIY>
A;Residues: 1-428,'D','430-444,'G','446-504 cMIY>
A;Cross-references: EMBL:X79320; NID:g515381; PIDN:CAA55888.1; PID:g515382
A;Cross-references: EMBL:X79320; NID:g515381; PIDN:CAA55888.1; PID:g515382
A;Cross-references: EMBL:X79320; Yamazoe, Y.; Kato, R.
J. Biochem. 107, 718-725, 1990
A;Title: Purification and characterization of four catalytically active termally related form:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arch. Biochem. Biophys. 298, 715-725, 1992
A;Title: Effect of dexamethasone and phenobarbital on ru
A;Reference number: S27107; MUID:93037516; PMID:1417000
A;Reference S27108
A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-36 CTEL>
A;Cross-references: EMBL:X62087
A;Cross-references: EMBL:X62087
A;Cross-references: EMBL:X62087
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C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text change
C;Accession: A2522; S27108; $4638; PX0033; PX0034; S30379
R;Gonzalez, F.J.; Song, B.J.; Hardwick, J.P.
Mol. Cell. Biol. 6, 2969-2976, 1986
A;Title: Pregnenolone 16-alpha-carbonitrile-inducible P-450 gene
A;Reference number: A2522; MUID:87064606; PMID:3785219
A;Accession: A25222
A;Molecule type: mRNA
A;Residues: 1-504 <GON>
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A25222
cytochrome P450 3A2 - rat
cytochrome P450 3A2 - rat
N;Alternate names: cytochrome P450CN2, pregnenolone 16-alpha-carbonitrile-inducible;
N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 09-Jul-2004
C;Accession: A25222; S27108; 546938; PX0032; PX0034; S30379
C;Accession: A25222; S27108; Hardwick, J.P.
R;Gonzalez, F.J.; Song, B.J.; Hardwick, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: PX0032; MUID:90375438; PMID:2398(A;Accession: PX0032
A;Accession: PX0032
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-21,'X',23-26,'X',28-29,'X',31-33 <NAG>A;Experimental source: liver, Sprague-Dawley male rata, A;Accession: PX0034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:PO5183; GB:M13646; NID:g203827; A;Note: the authors translated the codon GAC for residue 44! R;Telhada, M.B.; Pereira, T.M.; Lechner, M.C.
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   Query Match
Best Local S
Matches 346
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      Conservative
                                    74.9%;
72.2%;
      68;
   Score 1904.5; DB 2
Pred. No. 1.4e-134;
8; Mismatches 64;
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                                                              DB 2;
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R;Kirita, S.; Matsubara, T.
Arch. Biochem. Biophys. 307, 253-258, 1993
A;Title: cDNA cloning and characterization
A;Reference number: S39797; MUID:94099605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biochem. 116, 114-120, 1994
A;Title: A major glucocorticoid-inducible
A;Reference number: JX0334; MUID:95096005;
A;Accession: JX0334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Rattus norregicus (Norway ra
C;Date: 10-Mar-1994 #sequence_revision
C;Accession: JX0334; S39797
R;Komori, M.; Oda, Y.
J. Biochem. 116, 114-120, 1994
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JX0334
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A;Residues: 1-502 <KOM>
A;Cross_references: UNIPROT:Q06884;
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Date: 10-Mar-1994 #sequence_revision 28-Oct-1994
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIABDEEWKRLRSLLSPTFTSGKLKE
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                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                      74.8%;
72.5%;
                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                          Score 1902.5; DB Pred. No. 2e-134;
                                                                                                                                                                                                                            Mismatches
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; PMID:7528203
                                                                                                                                                                                                                                                                                       DB 2;
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A;Reference number: S39797; MUID:94099605; PMID:8274011
A;Reference number: RND S1979
A;Rolecule type: mRNA
A;Residues: 1-106,'D',108-502 KIR>
A;Residues: 1-106,'D',108-502 KIR>
A;Residues: 1-106,'D',108-502 KIR>
A;Residues: chochrome EMBL:D13912; NID:9220835; PIDN:BAA03008.1; PID:9220836; GB:X96721; C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology C;Keywords: chromoprotein; heme; iron; metalloprotein; monoxygenase; oxidoreductase; t;301-463/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 NTKKLLRFDFLDFFFLSITVFPFLIFILEVLNICVFPREVTNFLRKSVKRMKESRLEDTQ
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                                  YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
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FGTRTHGLFKKQGIPGPKPLPFFGTVLNYYMGLWKFDVECHKKYGKIWGLFDGQMPLFAI
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Search completed: July 8, 2005, 14:14:16 Job time: 43 secs

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Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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20: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

21: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Result
2542 2542 2501 249,94 249,2 237,2 223,3 2011.5 1958 1958	Score
100.0 100.0 98.4 98.1 96.4 93.3 87.8 87.8 77.0 77.0	Query Match
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Sequence 2, Appli Sequence 2, Appli Sequence 56, Appli Sequence 2, Appli Sequence 24, Appli Sequence 1079, Ap Sequence 3, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 2, Appli	Description

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588.5	•	•	•		594	10.	620.5	623	631	631	631	658.5	•	659.5	659.5	668.5	668.5	668.5	668.5	33	678.5	802	824.5		840.5	840.5	840.5	905	1620	1882	1882	1946.5	1956
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## ALIGNMENTS

RESULT 1  US-10-690-991-2  US-10-690-991-2  Sequence 2, Application US/10690991  Publication No. US20040243319A1  GENERAL INFORMATION:  APPLICANT: Tickle, Ian J  APPLICANT: Vonrhein, Clemens APPLICANT: Williams, Pamela A  APPLICANT: Williams, Pamela A  APPLICANT: Wilton, Stewart Brian  TITLE OF INVENTION: Crystal structure of cytochrome P450  FILIR REFERENCE: 620-282  CURRENT APPLICATION NUMBER: US/10/690,991  CURRENT APPLICATION NUMBER: US/01/063  PRIOR FILING DATE: 2002-10-25  PRIOR APPLICATION NUMBER: PCT/GB02/02668  PRIOR APPLICATION NUMBER: US 10/221,036  PRIOR APPLICATION NUMBER: US 10/221,036  PRIOR APPLICATION NUMBER: US 60/479,448  PRIOR PILING DATE: 2003-06-19  PRIOR APPLICATION NUMBER: US 60/479,448  PRIOR PILING DATE: 2003-06-19  NUMBER OF SEQ ID NOS: 6  SOFTWARE: Patentin version 3.1  SEQ ID NO 2  LENGTH: 485  TYPE: PRT  ORGANISM: Artificial sequence  FEATURE:  FEATURE:  OTHER INFORMATION: Human 3A4 P450 protein truncated in its N-terminal region to OTHER INFORMATION: delete the hydrophobic trans-membrane domain, and the region US-10-690-991-2																										
US/10690991 243319A1 J Clemens Pamela A Pamela A Pewart Brian ystal structure of cytochrome P450 ystal structure of cytochrome P450 ER: US 60/421,063 2-10-25 ER: US 60/421,036 2-05-30 ER: US 10/221,036 2-04-02 ER: US 60/479,448 3-06-19 6 ER: US 60/479,448 sion 3.1  sequence man 3A4 P450 protein truncated in its N-terminal relate the hydrophobic trans-membrane domain, and the placed by a short N-terminal sequence.	; CTHER INFORMATION: Hu ; OTHER INFORMATION: de ; OTHER INFORMATION: re ; OTHER OFFENDATION: re	ORGANISM: Artificial	; LENGTH: 485	<pre>; SOFTWARE: Patentin ver ; SEO ID NO 2</pre>	, NUMBER OF SEQ ID NOS:	; PRIOR FILING DATE: 200	PRIOR APPLICATION NUMB	; PRIOR FILING DATE: 200		; PRIOR APPLICATION NUMB	; PRIOR FILING DATE: 200	; PRIOR APPLICATION NUMB	; CURRENT FILING DATE:	; CURRENT APPLICATION NU	; FILE REFERENCE: 620-28	; TITLE OF INVENTION: Cr					; APPLICANT: Tickle, Ian	; GENERAL INFORMATION:	; Publication No. US20040	; Sequence 2, Application	US-10-690-991-2	RESULT 1
	uman 3A4 P450 protein truncated in its N-terminal reside the hydrophobic trans-membrane domain, and the splaced by a short N-terminal sequence.	sequence		rsion 3.1	6	03-06-19	BER: US 60/479,448	03-04-03	02-05-30	BER: PCT/GB02/02668	02-10-25	BER: US 60/421,063	2004-04-13	MBER: US/10/690,991	82	rystal structure of cytochrome P450	tewart Brian .	rren	Pamela A	Clemens	n CJ		0243319A1 · · · · · · · · · · · · · · · · · · ·	n US/10690991		

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APPLICANT: WILLIAMS, Pamela A
APPLICANT: WILLIAMS, Pamela A
TITLE OF INVENTION: Crystal Structure of Cytochrome P45
FILE REFERENCE: 620-305
CURRENT APPLICATION NUMBER: US/10/833,296
CURRENT FILING DATE: 2004-04-02
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: US 60/479,448
PRIOR FILING DATE: 2003-06-19
PRIOR FILING DATE: 2003-06-19
PRIOR FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: US 60/421,063
PRIOR PILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/306,873
PRIOR APPLICATION NUMBER: US 60/306,873
PRIOR PILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/306,874
PRIOR APPLICATION NUMBER: US 60/306,874
PRIOR APPLICATION NUMBER: US 10/690,991
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 10/690,991
PRIOR FILING DATE: 2002-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10833296
Publication No. US2005032119A1
GENERAL INFORMATION:
APPLICANT: Tickle, Ian J
APPLICANT: Vonrhein, Clemens
APPLICANT: Vinkovic, Dijana M
APPLICANT: Kirton, Stewart
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US-10-833-296-2
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Best Local Similarity
Matches 485; Conserv
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NUMBER: PCT/GB02/02668
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          Sequence 56, Application US/10313963A

Publication No. US20040002078A1

GENERAL INFORMATION:
APPLICANT: Boutell, Jonathan
APPLICANT: Hart, Darren
APPLICANT: Hart, Darren
APPLICANT: Blackburn, Jonathan
ITITLE OF INVENTION: Arrays
FILE REFERENCE: KIL-001
CURRENT APPLICATION NUMBER: US/10/313,963A
CCURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: US 60/335,806
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 60
PRIOR FILING DATE: 2002-09-16
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; TYPE: PRT
; ORGANISM: Artificial sequence
; PEATURE;
; PEATURE;
; OTHER INFORMATION: Human 3A4 P450 protein truncated in its N-terminal
; OTHER INFORMATION: to delete the hydrophobic trans-membrane domain, an
; OTHER INFORMATION: region replaced by a short N-terminal sequence.
US-10-833-296-2
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US-10-313-963A-56
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Best Local S
Matches 485
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 485
SOFTWARE: PatentIn version 3.1
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Local Similarity 100.0%;
ses 485; Conservative (
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Pred. No. 3.6e-218;
D; Mismatches 0;
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360 360

480 480 420 420 300

240 240 180

300

180 120 120 60

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Sequence 2, Application US/10146575

| Publication No. US20030059800A1
| GENERAL INFORMATION:
| APPLICANT: Lichter, Jay
| APPLICANT: Lichter, Jay
| APPLICANT: Guido, Marco
| TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
| FILE REFERENCE: SEQ-12P
| CURRENT APPLICATION NUMBER: US/10/146,575
| CURRENT FILING DATE: 2002-05-14
| PRIOR APPLICATION NUMBER: US/09/144,367
| PRIOR FILING DATE: 1998-08-31
| NUMBER: OF SEQ ID NOS: 58
| SOFTMARE: PASTESEQ for Windows Version 3.0
| SEQ ID NO 2
| LENGTH: 503
| TYPE: PRT
| ORGANISM: H. sapiens
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US-10-146-575-2
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                                                                                            Query Match
Best Local S
Matches 478
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Best Local Similarity 100.0%;
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LENGTH: 503
TYPE: PRT
ORGANISM: Homo Sapiens
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Similarity 99.8%;
78; Conservative
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                                                YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI
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TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
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                                                                                           Score 2494; DB 14;
Pred. No. 7.4e-214;
0; Mismatches 1;
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APPLICANT: Choe, Sunghwa
APPLICANT: Choe, Sunghwa
APPLICANT: Feldmann, Kenneth A.
TITLE OF INVENTION: DMF4 POLYNUCLEOTIDES, POLYPEPTIDES AND
FILE REFERENCE: 11696-070001
CURRENT APPLICATION NUMBER: US/10/804,772
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: US/09/502,426
PRIOR APPLICATION NUMBER: US/09/502,426
PRIOR FILING DATE: 2000-02-11
PRIOR PILLING DATE: 1999-02-11
PRIOR PILLING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US 60/119,658
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-804-772-24
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 24
LENGTH: 504
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Azpiroz, Ricardo
APPLICANT: Choe, Sunghwa
APPLICANT: Feldmann, Kenne
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                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
 205
                                  183
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                     ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT
                                                                                      MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                                                                      TDPDMIKLVLVKECYSVFTNREPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
                                                                                                                                                        TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE
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ENTKKLLREDFILDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKAVKRMKESRLEDT
                                                                    MVPIIAQYGDVLVRNLRRERETGKPVTLKDVFGAYSMDVITSSSFGVNVDSLNNPQDPLV
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97.9%;
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Pred. No. 7e-210;
4; Mismatches 5;
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APPLICANT: Edgerton, Michael D
ITITLE OF INVENTION: TRANSGERIC PLANTS WITH IM
FILE OF INVENTION: TRANSGERIC PLANTS WITH IM
CHILLE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILLING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
VUMBER OF SEQ ID NOS: 24149
SEQ ID NO 1079
LENGTH: 503
TYPE: PRT
ORGANISM: Macaca fascicularis
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US-10-732-923-1079
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Best Local (
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MRFALMAMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
                                                                    GMFI PKGVVVMI PSYALHRDPKYWTEPEKFLPERFSKKNKONI DPYI YTPFGSGPRNCIG
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Pred. No. 5.9e-203;
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Sequence 3, Application US/09957997
Patent No. US20020150915A1
GENERAL INFORMATION:
APPLICANT: Berkenstam, Anders
APPLICANT: Berkenstam, Anders
APPLICANT: Berkenstam, Arders
APPLICANT: Blomquist, Patrik
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-046001
CURRENT APPLICATION NUMBER: US/09/957,997
CURRENT FILING DATE: 2001-09-21
EARLIER APPLICATION NUMBER: SE 0003393-6
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER APPLICATION NUMBER: 60/238,895
EARLIER FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 503
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; ORGANISM: Homo
US-09-957-997-3
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Best Local Similarity
Matches 425; Conserv
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GMFI PKGVVVMI PSYALHRDPKYWTEPEKFLPERFSKKUKDNI DPYI YTPFGSGPRUC I G
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                                                            GMFIPKGVVVMIPSYVLHHDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG
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88.7%;
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Pred. No. 1.6e-190;
7; Mismatches 27;
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RESULT 8
US-10-626-66
; Sequence 66, Application US/10626686
; Publication No. US20050074842A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
APPLICANT: Kimura, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
; TITLE OF INVENTION: DOMAINS AND DNAS ENCODING THESE PRO
; FILE REPERENCE: GIN-6706CPUS

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Sequence 7, Application US/10274694
Publication No. US20030143589A1
GENERAL INFORMATION:
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BRUNS, Christopher M.
APPLICANT: DAS, Debopriya
APPLICANT: DING, Li
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: GANDHI, Ameena R.
APPLICANT: HAPALIA, April J.A.
APPLICANT: KEARNEY, Liam
APPLICANT: KHAN, Farrah A.
APPLICANT: KHAN, Farrah A.
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US-10-274-694-7
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CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/445,258A
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/US98/02445
PRIOR FILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: JP 9-144948
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 67
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local
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APPLICANT:
APPLICANT:
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APPLICANT:
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TYPE: PRT
ORGANISM: Macaca f
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                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                            MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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              LAL, Preeti G.
LEE, Ernestine A.
LU, Dynng Aina M.
LU, Yan
NGUYEN, Danniel B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVPIIAKYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
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PATTERSON, Chandra
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Pred. No. 9.7e.
16; Mismatches
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CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 60/221,837
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/220,037
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/218,948
PRIOR APPLICATION NUMBER: 60/218,948
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US01/21324
PRIOR APPLICATION NUMBER: 60/216,804
PRIOR APPLICATION NUMBER: 60/216,804
PRIOR FILING DATE: 2000-07-07
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SOFTWARE: PERL
SEQ ID NO 7
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Best Local
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte II
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TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
443
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                                              GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
                                                                                                                                                             NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKXXKDNIDPYIYTPFGSGPRNCI
                                                                                                                                                                                                                                                     HPDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEI
                                                                                                                                                                                                                                                                                                HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI
                                                                                                                                                                                                                                                                                                                                                                             KQKHRVDPFQQMIDSQNSKETKSHKALSDLELVAQSIIIFAAYDTTSTTLPFIMYELAT
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GMRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG
                                                                                                                            NGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCI
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YUE, Henry
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RING, Huijun Z.
SANJANWALA, Madhusu
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WG, Junming
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Pred. No. 5.9e-166;
2; Mismatches 63;
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PRIOR APPLICATION NUMBER: US 60/216,804
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/218,948
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/220,037
PRIOR APPLICATION NUMBER: US 60/220,037
PRIOR APPLICATION NUMBER: US 60/221,837
PRIOR APPLICATION NUMBER: US 60/221,837
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NO 7
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APPLICANT: BRUNS, Christopher M.; DAS, Debopriya Das;
APPLICANT: BRUNS, Christopher M.; DAS, Debopriya Das;
APPLICANT: DING, I, ELLIOTT, Vicki S.; GANDHI, Ameena R.;
APPLICANT: HAFALIA, April; KRANNEY, Liam; KHAN, Farrah A.;
APPLICANT: LAL, Preeti; LEE, Ernestine A.; LU, Dyung Aina M.;
APPLICANT: LU, Yan; DANNIEL, Nguyen B.; ARVIZU, Chandra S.;
APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: SANJANWALLA, Madhu S.; TANG, Y. Tom;
APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael;
APPLICANT: TRIBOULEY, Catherine M.; WALIA, Narinder K.;
APPLICANT: XU, Yuming; YANG, Junming; YAO, Monique G.; YUE, Henry
TITLE OF INVENTION: Drug Metabolizing Enzymes
FILE REFERENCE: PI-0.51 USN
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; OTHER INFORMATION: Incyte ID No: 7476298CD1
US-10-332-448-7
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US-10-332-448-7
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Best Local S
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CURRENT FILING DATE: 2003-01-07
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                                                                                                                                                                                                                                                                                                                                                                               NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
                                                                                                                                                                                                                                       TQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT
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GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
                                                                                                                            HPDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEI
                                                                                                                                                                                                                 KQKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELAT
                                        NGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCI
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; Pred. No. 5.9e-166;
52; Mismatches 63;
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RESULT 12
US-10-112-944-432
; Sequence 432, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:

APPLICANT:

Zhang, Jie Ren, Feiyan Xue, Aidong

APPLICANT: Tang, Y. Tom APPLICANT: Yang, Yonghong APPLICANT: Weng, Gezhi

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NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 503
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Publication No. US20020160479A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wojnowski, Leszek
APPLICANT: Wojnowski, Leszek
APPLICANT: Biselt, Regina
APPLICANT: Eiselt, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
FILE REFERENCE: 310115.401D1
CURRENT APPLICATION NUMBER: US/10/007,814
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ORGANISM: Homo
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MRFALTNIKLAVIRALQNESFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG
                      MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
                                                                             GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
                                                                                                                                                                                  KMMKKLLKLDFLDFLLLISLFPFLTFVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK
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                                                                                                                          PDVQQKLQBEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN
                                                                                                                                            PDVQQKLQEBIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVBIN
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CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT PILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR PILLING DATE: 2000-01-25
PRIOR PILLING DATE: 2000-02-03
PRIOR PILLING DATE: 2000-02-03
PRIOR PILLING DATE: 2000-02-03
PRIOR PILLING DATE: 2000-02-03
PRIOR PILLING DATE: 2000-03-07
PRIOR PILLING DATE: 2000-03-07
PRIOR PILLING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR PILLING DATE: 2000-03-11
PRIOR PILLING DATE: 2000-03-11
PRIOR PILLING DATE: 2000-03-11
PRIOR PILLING DATE: 2000-03-11
PRIOR PILLING DATE: 2000-04-18
PRIOR PILLING DATE: 2000-05-18
PRIOR PILLING DATE: 2000-05-18
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Best Local S
Matches 364
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SEQ ID NO 432
LENGTH: 503
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APPLICANT:
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APPLICANT: Wang, Zhiwei
TITLE OP INVENTION: No. US20040048249Alel Nucleic
TITLE OP INVENTION: Secreted Polypeptides
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                                                                                           GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
                                                                                                                                                                                                                                                                             KNMKKLLKLDFLDPFLLLIALFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK
                                                                                                                                                                                                                                                                                               ENTKKLLRFDFLDFFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
                                                                                                                                                                                                                                                                                                                                                                  MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
                                                             GVFIPKGLAVMVPIYALHHDPKYWTEPBKFCPBRFSKQNKDSIDLYRYIPFGAGPRNCIG
                                                                                                                                                          PDVQQKLQBEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFFIAMRLERVCKKDVEIN 362
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Wang, Dunrui
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Pred. No. 8.9e-166;
0; Mismatches 64;
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RESULT

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RESULT 14 US-10-274-694-16

Sequence 16, Application US/10274694 Publication No. US20030143589A1 GENERAL INFORMATION:

APPLICANT: BAUGHN, Mariah R.
APPLICANT: BRUNS, Christopher M.
APPLICANT: DAS, Debopriya
APPLICANT: DING, Li
APPLICANT: BLLIOTT, Vicki S.
APPLICANT: GAUDHI, Ameena R.
APPLICANT: HAPALIA, April J.A.

ELLIOTT, Vicki (GANDHI, Ameena I HAFALIA, April (KEARNEY, Liam

APPLICANT: APPLICANT: APPLICANT:

KHAN, Farrah A. LAL, Preeti G.

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Publication No. US20020160479A1

GENERAL INFORMATION:
APPLICANT: Wojnowski, Leszek
APPLICANT: Gellner, Klaus
APPLICANT: Eiselt, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450:
TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
FILE REFERENCE: 310115.401D1
CURRENT APPLICATION NUMBER: US/10/007,814
CURRENT FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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TYPE: PRT
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Similarity 76.0%;
GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
                                                         PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN
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Pred. No. 6.3e-165;
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; OTHER INFORMATION: Incyte ID No. US20030143589A1 7478053CD1
US-10-274-694-16
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PRIOR APPLICATION NUMBER: 60/221,837
PRIOR FILING DATE: 2000-07-28
PRIOR PPLICATION NUMBER: 60/220,037
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/218,948
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PRIOR DATE: 2000-07-14
PRIOR PRIOR DATE: 2001-07-05
PRIOR FILING DATE: 2011-07-05
PRIOR FILING DATE: 2011-07-05
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Best Local
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SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DRUG METABOLIZING ENZYMES FILE REFERENCE: PI-0151 USA CURRENT APPLICATION NUMBER: US/10/274,694 CURRENT FILING DATE: 2002-10-18
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ORGANISM: Homo
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                                                                   MYELATHPDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVC
                                                                                                     MYELATHPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVC
                                                                                                                                                               ESRLEDTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFI
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                                 KKDVEINGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGS
                                                                                                                                           ESRLKDKOKHRVDFFQQMIDSONSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFI
                                                                                                                                                                                                                      NPQDPFLKNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMK
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KKDIEINGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGA
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YUE, Henry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YANG, Junming
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THORNTON, Michael B.
TRIBOULEY, Catherine M.
WALIA, Narinder K.
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73.6%;
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Pred. No. 3.7e-159;
64; Mismatches 68;
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APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;
APPLICANT: BRINS, Christopher M.; DAS, Debopriya Das;
APPLICANT: DING, Li; ELLIOTT, Vicki S.; GANDHI, Ameena R.;
APPLICANT: HAFALIA, April; KEARNEY, Liam; KHAN, Farrah A.;
APPLICANT: LAL, Preeti; LEE, Ernestine A.; LU, Dyung Aina M.;
APPLICANT: LU, Yan; DANNIEL, Nguyen B.; ARVIZU, Chandra S.;
APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: SANJANWALA, Madhu S.; TANG, Y. Tom;
APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael;
APPLICANT: TRIBOULEY, Catherine M.; WALIA, Narinder K.;
APPLICANT: XU, Yuming; YANG, Jumming; YAO, Monique G.; YUE, Henry
TITLB OF INVENTION: Drug Metabolizing Enzymes
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7478053CD1
US-10-332-448-16
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PRIOR APPLICATION NUMBER: US 60/216,804
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/218,948
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/220,037
PRIOR APPLICATION NUMBER: US 60/221,837
PRIOR APPLICATION NUMBER: US 60/221,837
PRIOR APPLICATION NUMBER: US 60/221,837
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PER
SEQ ID NO 16
LENGTH: 508
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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SOFTWARE: PERL Program
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MYELATHPOVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVC
                                                                      ESRLEDTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFI
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                                          ESRLKDKQKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFI
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Search Job ti	B	Ş	망	გ	ర్జ	Ş	문
Search completed: July 8, 2005, 14:30:06 Job time : 170 secs	503 GITSG 507	476 GTVSG 480	443 GPRNCIGMRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRD 502	416 GPRNCIGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRD 475	383 KKDIEINGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGA 442	356 KKOVEINGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGS 415	

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